Circulation
JOURNAL OF THE AMERICAN HEART ASSOCIATION

American Heart Association®
Learn and Live℠

Differential Cardiac Remodeling in Preload Versus Afterload

Karl Toischer, Adam G. Rokita, Bernhard Unsöld, Wuqiang Zhu, Georgios Kararigas, Samuel Sossalla, Sean P. Reuter, Alexander Becker, Nils Teucher, Tim Seidler, Cornelia Grebe, Lena Preuß, Shamindra N. Gupta, Kathie Schmidt, Stephan E. Lehnart, Martina Krüger, Wolfgang A. Linke, Johannes Backs, Vera Regitz-Zagrosek, Katrin Schäfer, Loren J. Field, Lars S. Maier and Gerd Hasenfuss

Circulation 2010;122;993-1003; originally published online Aug 23, 2010;
DOI: 10.1161/CIRCULATIONAHA.110.943431
Circulation is published by the American Heart Association. 7272 Greenville Avenue, Dallas, TX 72514

Differential Cardiac Remodeling in Preload Versus Afterload

Karl Toischer, MD*; Adam G. Rokita, MD*; Bernhard Unsöld, MD; Wuqiang Zhu, MD, PhD;
Georgios Kararigas, PhD; Samuel Sossalla, MD; Sean P. Reuter, TA; Alexander Becker, MD;
Nils Teucher, MD; Tim Seidler, MD; Cornelia Grebe, PhD; Lena Preuß, MSc;
Shamindra N. Gupta, MSc; Kathie Schmidt, MSc; Stephan E. Lehnart, MD; Martina Krüger, PhD;
Wolfgang A. Linke, PhD; Johannes Backs, MD; Vera Regitz-Zagrosek, MD; Katrin Schäfer, MD;
Loren J. Field, PhD; Lars S. Maier, MD*; Gerd Hasenfuss, MD*

Background—Hemodynamic load regulates myocardial function and gene expression. We tested the hypothesis that afterload and preload, despite similar average load, result in different phenotypes.

Methods and Results—Afterload and preload were compared in mice with transverse aortic constriction (TAC) and aortocaval shunt (shunt). Compared with sham mice, 6 hours after surgery, systolic wall stress (afterload) was increased in TAC mice (+40%; $P<0.05$), diastolic wall stress (preload) was increased in shunt (+277%; $P<0.05$) and TAC mice (+74%; $P<0.05$), and mean total wall stress was similarly increased in TAC (69%) and shunt mice (67%) (P=NS, TAC versus shunt; each $P<0.05$ versus sham). At 1 week, left ventricular weight/tibia length was significantly increased by 22% in TAC and 29% in shunt mice (P=NS, TAC versus shunt). After 24 hours and 1 week, calcium/calmodulin-dependent protein kinase II signaling was increased in TAC. This resulted in altered calcium cycling, including increased L-type calcium current, calcium transients, fractional sarcoplasmic reticulum calcium release, and calcium spark frequency. In shunt mice, Akt phosphorylation was increased. TAC was associated with inflammation, fibrosis, and cardiomyocyte apoptosis. The latter was significantly reduced in calcium/calmodulin-dependent protein kinase IIδ-knockout TAC mice. A total of 157 mRNAs and 13 microRNAs were differentially regulated in TAC versus shunt mice. After 8 weeks, fractional shortening was lower and mortality was higher in TAC versus shunt mice.

Conclusions—Afterload results in maladaptive fibrotic hypertrophy with calcium/calmodulin-dependent protein kinase II–dependent altered calcium cycling and apoptosis. Preload is associated with Akt activation without fibrosis, little apoptosis, better function, and lower mortality. This indicates that different loads result in distinct phenotype differences that may require specific pharmacological interventions. **(*Circulation*. 2010;122:993-1003.)**

Key Words: afterload ■ apoptosis ■ CaM kinase ■ heart failure ■ hemodynamics ■ preload ■ remodeling

In the heart, hemodynamic load is a critical regulator of myocardial function, gene expression, and phenotype appearance.[1] Specific structures involved in perception of hemodynamic load have been identified, and influencing or deleting these structures has been associated with cardiac dysfunction and disease.[2] Two types of load can be differentiated. Preload builds up during diastolic filling and stretches cardiomyocytes. This results in immediate recruitment of contractile units and increased cardiac performance through the Frank-Starling mechanism. In addition, proteins such as titin and associated molecules are stretched with subsequent effects on myocardial elasticity and gene expression.[3] Systolic force matching afterload is generated by each cardiomyocyte to produce cardiac stroke work against vascular resistance. This is accomplished by the contractile protein complex. During ejection, preload declines and titin is unloaded. Both preload and afterload influence load-dependent ion channels and intracellular ion concentrations,[4] which in turn may also influence cardiac function and gene expression. From a hemodynamic point of view, afterload-mediated concentric hypertrophy was considered beneficial because of stress compensation through increased wall thickness according to

---

Received June 5, 2009; accepted June 24, 2010.

From the Department of Cardiology and Pneumology, Heart Center, Georg-August University, Goettingen, Germany (K.T., A.G.R., B.U., S.S., A.B., T.S., C.G., L.P., S.N.G., K.S., S.E.L., K.S., L.S.M., G.H.); Wells Center for Pediatric Research and Krannert Institute of Cardiology, Indiana University School of Medicine, Indianapolis (W.Z., S.P.R., L.J.F.); Institute of Gender in Medicine, Charité-Universitätsmedizin Berlin, Berlin, Germany (G.K., V.R.-Z.); Department of Cardiac Surgery, Georg-August University, Goettingen, Germany (N.T.); Department of Cardiovascular Physiology, Ruhr University, Bochum, Germany (M.K., W.A.L.); and Department of Internal Medicine III, University of Heidelberg, Heidelberg, Germany (J.B.).

*Drs Toischer and Rokita contributed equally to this study, and Drs Maier and Hasenfuss contributed equally to this study.

The online-only Data Supplement is available with this article at http://circ.ahajournals.org/cgi/content/full/CIRCULATIONAHA.110.943431/DC1.

Correspondence to Gerd Hasenfuss, MD, Department of Cardiology and Pneumology, Georg-August-University Goettingen, Robert-Koch-Str. 40, 37075 Göttingen, Germany. E-mail hasenfus@med.uni-goettingen.de

Circulation **is available at http://circ.ahajournals.org** **DOI: 10.1161/CIRCULATIONAHA.110.943431**

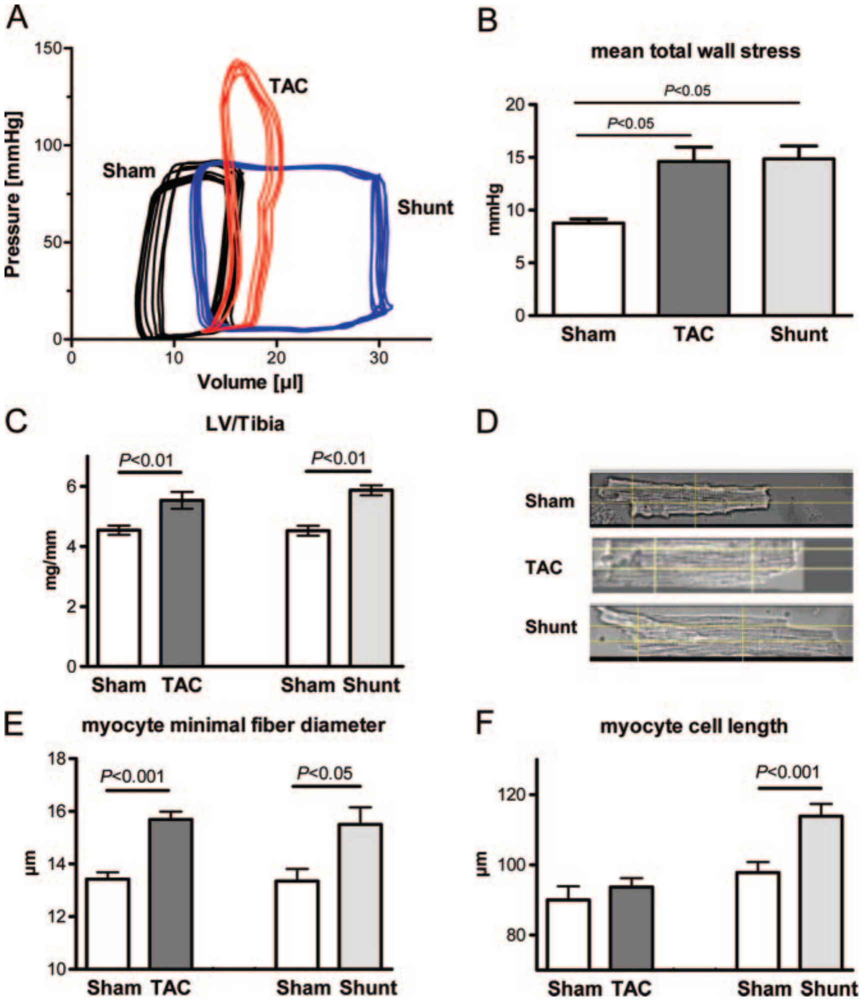

Figure 1. Hemodynamics in sham, TAC, and shunt groups 6 hours after intervention (A, B) and hypertrophy 7 days after intervention (C through F). A, Examples of pressure-volume loops. B, Mean total wall stress (n=3 per group). C, Left ventricular (LV) weight normalized to tibia length 7 days after intervention (n=8/10/6/6). D, Example of single cardiomyocytes isolated 7 days after intervention. E, Cell width measured by minimal fiber diameter (animals: n=5/6/5/6). F, Cell length measured in isolated cardiomyocytes (animals: n=5/7/4/4).

the law of Laplace.[5] In contrast, preload-mediated eccentric hypertrophy was considered maladaptive because of uncompensated wall stress. However, cardiac geometry and macroscopic phenotype are only one aspect. Myocardial hypertrophic phenotype (ie, the protein composition of the myocardium) is another, and there is good evidence that the latter may be more relevant to the transition to heart failure.[6]

Clinical Perspective on p 1003

In previous studies in isolated muscle preparations, we showed that preload and afterload differentially regulate expression of fetal genes.[7,8] The present study was performed to compare differences in phenotypes, signaling, and gene expression of preload- and afterload-induced hypertrophy in vivo. Therefore, we used the aorta–vena cava mouse fistula model (shunt), which generates volume overload and predominantly increased preload, and the transverse aortic constriction (TAC) model, which generates pressure overload and reflects increased afterload. Shunt and TAC mice were graded to match average load, measured as average left ventricular wall stress. Our data show that eccentric hypertrophy in shunt mice is more beneficial than concentric hypertrophy in TAC mice with increased inflammation, fibrosis, and cardiomyocyte apoptosis. The shunt model is associated with Akt activation, whereas the TAC model is associated with altered calcium cycling and calcium/calmodulin-dependent protein kinase II (CaMKII)[9] activation.

Methods

Only a short description of Methods is given here. An expanded version can be found in the online-only Data Supplement.

Animal Experiments and In Vivo Characterization

The investigation conforms to the *Guide for the Care and Use of Laboratory Animals* (National Institutes of Health publication No. 85–23, revised 1996). In 12-week-old female mice, volume overload was induced by the creation of a shunt between the aorta and vena cava inferior. Pressure overload was induced by TAC. Female mice were used because of high mortality in male mice. Echocardiography, in vivo hemodynamic measurements, cardiomyocyte isolation, cardiomyocyte shortening, calcium measurements, and patch-clamp experiments were performed with standard protocols.

Molecular Analysis

Protein and gene expression were measured with standard protocols of Western immunoblots and quantitative real-time polymerase chain reaction (Biorad iQ-Cycler). Fibrosis, cardiomyocyte apoptosis, and inflammation were quantified in histological sections. For measurement of the cell cycle rate, ^{3}H-thymidine autoradiography was measured. The 11.0 miRCURY LNA microRNA array (Exiqon, Denmark) was used for microRNA, and the Affymetrix mouse 430 2.0 GeneChip array was used for gene expression analysis. Gene expression microarray data have been deposited in the ArrayExpress database (accession No. E-MEXP-2498).

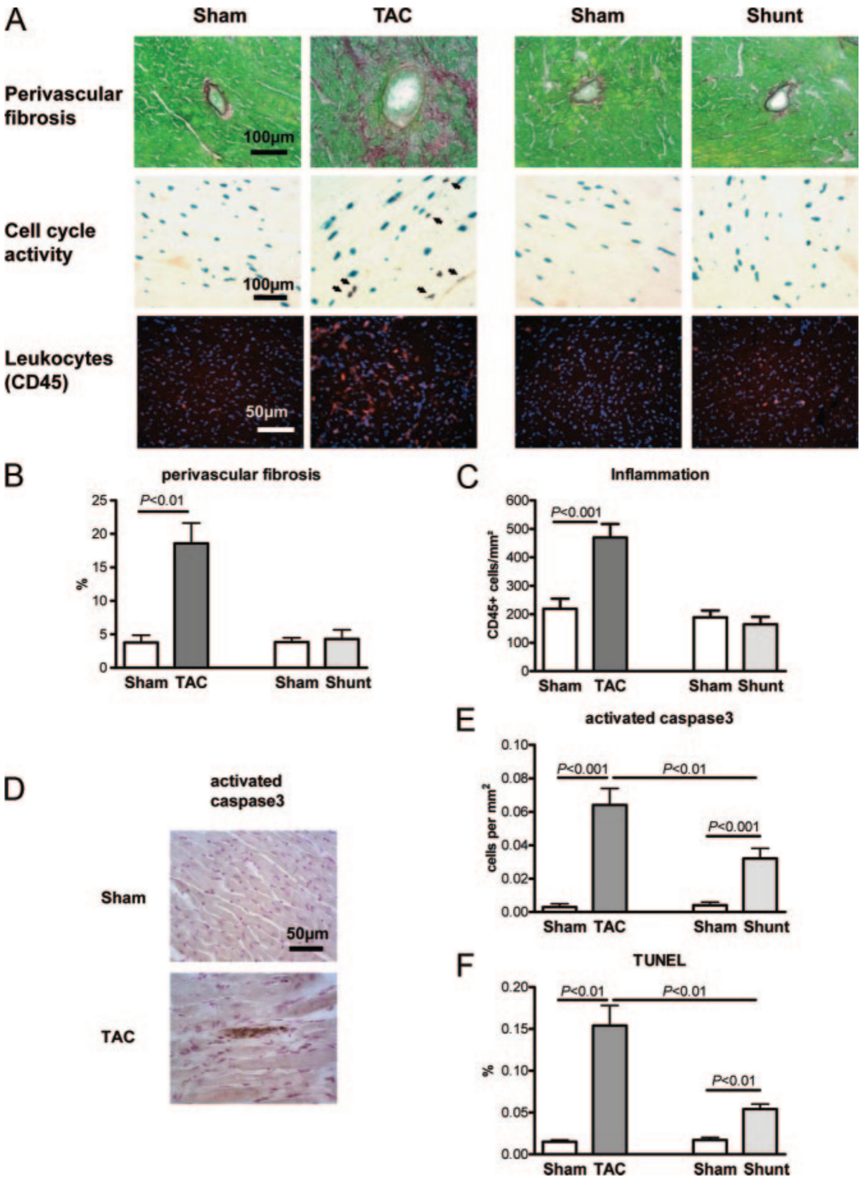

Figure 2. Histological analysis of sham, TAC, and shunt animals 7 days after intervention (n=5/6/5/6). A, Histological sections of staining for fibrosis (Sirius red), cell cycle rate (^{3}H-thymidine injection in α-MHC-nLAC transgenic mice; blue=cardiomyocyte nuclei, black=cell cycle activity), and inflammation (anti-CD45 immunohistochemistry; red=leucocytes, blue=cell nuclei). B, Bar graphs showing perivascular fibrosis. C, Bar graphs showing inflammation. D, Example of active caspase3 staining in sham and TAC. E, Cardiomyocyte apoptosis rate by activated caspase 3 staining. F, Apoptosis rate by terminal deoxynucleotidyl transferase dUTP nick end labeling (TUNEL) (number of positive cells per 100 nuclei).

Calculation and Statistical Analysis

Data are presented as mean±SEM. $P<0.05$ was considered statistically significant. Gene- and protein-expression and electrophysiological experiments were analyzed statistically with the use of unpaired Student *t* test, 1-way ANOVA on ranks (Dunn's method), or 1-way ANOVA followed by the Tukey post hoc test, where appropriate. Survival was analyzed by Kaplan-Meier and Fisher tests. Wall stress was calculated according to the law of Laplace. Raw microarray data were imported into R version 2.9.1 and analyzed with Bioconductor packages. Pathway analysis was performed by the gene set enrichment analysis approach with the use of the Category and GSEABase Bioconductor packages, querying the Kyoto Encyclopedia of Genes and Genomes pathway database (for references, see the statistical section of the online-only Data Supplement). The numbers of animals or cells are shown in the figure legends in the following order: n=sham (TAC)/TAC/sham (shunt)/shunt.

Results

Hemodynamic Function and Wall Stress

Conductance catheter pressure volume analysis 6 hours after respective surgical procedures (Figure 1A) showed that left ventricular systolic pressure was increased in the TAC group (+41%; $P<0.05$), and left ventricular end-diastolic pressure and volume were increased in the shunt group (+97%; $P<0.05$; Figure I in the online-only Data Supplement). Wall stress was calculated at 4 time points during the cardiac cycle (midsystolic, end-systolic, mid-diastolic, end-diastolic; Figure IIA in the online-only Data Supplement). In the TAC group, midsystolic wall stress was increased by 40% ($P<0.05$; Figure IIB in the online-only Data Supplement), and end-diastolic wall stress was increased by 277% in the shunt group ($P<0.05$) and by 74% in the TAC group (each $P<0.05$; Figure IIE in the online-only Data Supplement). Mean total wall stress during 1 cardiac contraction-relaxation cycle yielded similar values for TAC and shunt groups (TAC, 69%; shunt, 67%; each $P<0.05$ versus sham; Figure 1B), which indicates similar average load elevation immediately after surgery in both models. Echocardiographic measurements 24 hours after intervention confirmed left ventricular dilatation in the shunt group by increased left ventricular

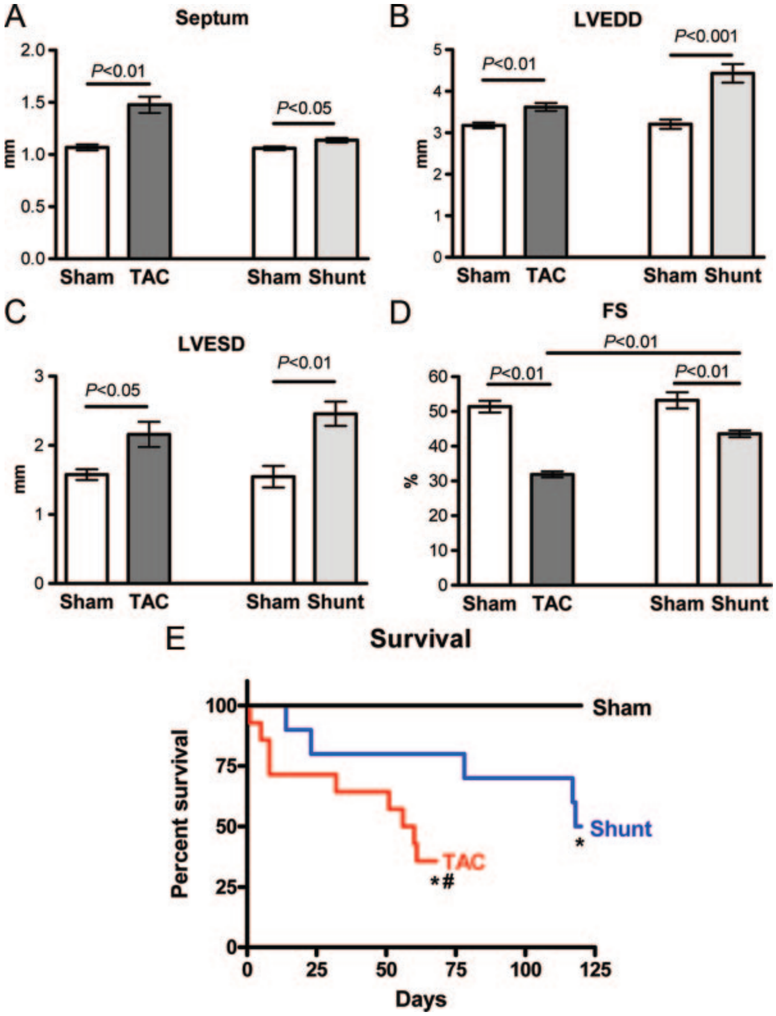

Figure 3. Echocardiographic measurements 8 weeks after intervention and survival in sham, TAC, and shunt animals, A, Septum width. B, Left ventricular end-diastolic diameter (LVEDD). C, Left ventricular end-systolic diameter (LVESD). D, Fractional shortening (FS). E, Kaplan-Meier survival in TAC and shunt animals (*$P<0.01$ vs sham; #$P<0.05$ vs shunt).

end-diastolic diameter ($P<0.05$), whereas fractional shortening was not changed at this time point (Figure III in the online-only Data Supplement).

Remodeling and Left Ventricular Hypertrophy

After 1 week, left ventricular hypertrophy as indicated by left ventricular weight per tibia length was increased similarly in both models, being concentric in the TAC group and eccentric in the shunt group (TAC, +22%; shunt, +29%; each $P<0.01$; TAC versus shunt, P=NS; Figure 1C). Cardiomyocyte minimal fiber diameter was increased in both models (Figures 1D and 1E), whereas cardiomyocyte length was increased only in the shunt group (Figures 1D and 1F). Echocardiographic characterization is shown in the online-only Data Supplement (Figure IV in the online-only Data Supplement). At this time point, myocardial function was not reduced in either model (Figure IVD in the online-only Data Supplement).

Hypertrophy in the TAC group was associated with a significant increase in myocardial fibrosis (perivascular fibrosis +490%; $P<0.01$; Figure 2A and 2B). Cell cycle rate showed a clear increase in TAC in the noncardiomyocytes but not in the shunt group (Figure 2A; for discrimination of cardiomyocytes and noncardiomyocytes, nuclear-ßGAL transgenic mice were used). This suggests that increased fibrosis in the TAC group resulted in part from fibroblast proliferation. In addition, inflammation was increased in TAC by 114% ($P<0.001$; Figure 2A and 2C). In the shunt group, fibrosis and inflammation were not elevated (Figure 2A through 2C). Cardiomyocyte apoptosis was elevated in both the TAC and shunt groups, but it was significantly higher in the TAC group (Figure 2D through 2F).

Long-Term Myocardial Function and Mortality

Eight weeks of increased load were associated with a moderate increase in septum thickness in the shunt group (+7%; $P<0.05$) and a large increase in TAC (+39%; $P<0.01$; Figure 3A). End-diastolic diameter was increased in the TAC group by 14% ($P<0.05$) and in the shunt group by 38% ($P<0.01$; Figure 3B). Fractional shortening was considerably reduced in the TAC group (−38%; $P<0.01$), whereas it was only slightly reduced in the shunt group (−18%; $P<0.01$ versus sham, $P<0.01$ versus TAC; Figure 3D). After 8 weeks, the percentage of surviving animals was significantly lower in the TAC group (4/13) than in the shunt group (7/10; $P<0.05$). In addition, Kaplan-Meier analysis yielded significantly higher mortality in the TAC versus the shunt group ($P<0.05$; Figure 3E).

Table 1. Expression of Hypertrophic Genes in TAC and Shunt Groups

	24 Hours		7 Days	
	TAC	Shunt	TAC	Shunt
BNP/ GAPDH	507.3±159.7*	41.2±51.1	383.9±63.3*	44.2±30.6
α-MHC/ GAPDH	−0.8±29.4	−3.9±29.1	−41.9±16.7*	−17.5±20.5
β-MHC/ GAPDH	81.3±27.5*	14.3±25.0	229.3±71.1†	17.6±32.1
SERCA/ GAPDH	−15.5±8.9	−1.7±6.7	−17.7±9.8	−12.8±7.9
PLB/ GAPDH	0.3±1.1	−12.4±8.1	−0.0±0.5	−16.3±11.8
NCX/ GAPDH	32.8±12.4*	7.1±13.8	17.3±13.9	3.2±11.6
RYR2/ GAPDH	−10.1±11.9	−6.7±11.3	−21.9±10.5	−15.6±10.3

Values are percentages. MicroRNA expressions of hypertrophy-associated and calcium-regulating proteins in TAC and shunt groups 24 hours (n=6/6/6/7) and 7 days (n=8/10/7/7) after intervention are shown. Changes are normalized to the corresponding sham.

*$P<0.05$.

†$P<0.01$.

Load-Dependent Regulation of Gene Expression and Signal Transduction Pathways

Left ventricular gene expression and protein phosphorylation were analyzed 24 hours and 7 days after intervention to show persistent activation (Tables 1 and 2). Brain natriuretic peptide (BNP) was upregulated at both time points only in the TAC group (24 hours, +507%, $P<0.05$; 7 days, +384%, $P<0.05$; Table 1). An isoform shift from α-myosin heavy chain (MHC) to β-MHC at these time points occurred in the TAC but not in the shunt model (Table 1). Upregulation of ß-MHC gene expression in the TAC model already occurred after 24 hours. The expression of SERCA and the other calcium-regulated proteins was not changed at 24 hours and 7 days after intervention in both models, with the exception of a transient upregulation of NCX in TAC (Table 1).

CaMKII, histone deacetylase, Akt, GSK3ß, and mitogen-activated protein kinase expression and activation were measured with specific antibodies as well as with phosphospecific antibodies (Figures V and VI in the online-only Data Supplement). If protein expression was not altered, the ratio of phosphorylated protein to total protein is shown. When total protein expression was altered, phosphorylated protein normalized to GAPDH as well as the ratio of phosphorylated protein to total protein and total protein expression to GAPDH is shown. An absolute increase of phosphorylated protein is considered to reflect increased biological activity.

Increased biological activity at 24 hours and 7 days was seen only for CaMKII and Akt. In TAC, the biological CaMKII activity was increased after 24 hours and 7 days by 78% and 82%, respectively (Figure 4A and 4B and Table 2). None of these changes were observed in the shunt group (Figure 4A and 4B and Table 2), whereas Akt phosphorylation was increased in the shunt group exclusively (24 hours, +70%, $P<0.05$; 7 days, 41%, $P<0.05$; Table 2).

Table 2. Activation of Signaling Pathways in TAC and Shunt Groups

	24 Hours		7 Days	
	TAC	Shunt	TAC	Shunt
P-CaMKII/ GAPDH	77.5±28.1*	−8.9±18.6	81.5±32.6*	−20.0±16.7
CaMKII/ GAPDH	23.7±9.1	−10.0±14.3	23.7±9.1*	−10.0±14.3
P-CaMKII/ CaMKII	66.3±22.9^{+}	3.3±22.3	28.6±22.9	−9.2±16.4
P-Akt/Akt	9.3±18.5	70.2±30.4*	22.3±18.5	41.3±17.8*
P-p38/ GAPDH	8.1±20.4	44.7±18.4*	15.8±19.9	−20.6±14.0
p38/ GAPDH	−26.0±12.4	−23.1±9.6*	−35.1±8.9*	−29.4±12.4*
P-p38/ p38	47.8±19.7*	124.5±36.7†	92.9±30.0*	0.6±13.7
P-ERK/ ERK	74.3±29.2*	4.2±19.5	−61.4±23.6*	17.5±35.4
P-JNK/ JNK	0.1±25.4	0.1±15.1	−50.7±36.0	82.3±38.5
P-HDAC/ CS			107.4±37.8*	7.7±17.4
P-GSK3ß/ GSK3ß	4.0±9.5	26.3±11.3*	−7.1±11.9	−8.3±16.2
MCIP/ GAPDH	−7.6±2.1	3.1±4.0	454.7±105.3*	55.3±46.7

Values are percentages. Activations of signaling pathways in TAC and shunt groups 24 hours and 7 days after intervention are shown. Changes are expressed relative to the corresponding sham (n=6 per group). Normalization is done per GAPDH or per calsequestrin (CS) or per respective protein. HDAC indicates histone deacetylase; MCIP, myocyte-enriched calcineurin-interacting protein.

*$P<0.05$.

†$P<0.01$.

The other kinases studied were not consistently activated at 24 hours and 7 days: p38 phosphorylation but not total biological activity was increased at both time points in the TAC group (Table 2). Changes in ERK phosphorylation also occurred only in the TAC group (24 hours, +74%, $P<0.05$; 7 days, −61%, $P<0.05$; Table 2). In addition, histone deacetylase phosphorylation was increased only in the TAC group (Table 2). GSK3β phosphorylation was increased in the shunt group after 24 hours (+26%, $P<0.05$; Table 2). mRNA expression of myocyte-enriched calcineurin-interacting protein as an indicator of calcineurin activity was selectively upregulated after 7 days in TAC (myocyte-enriched calcineurin-interacting protein, +454%, $P<0.05$; Table 2).

Analysis of left ventricular human heart samples from patients with aortic stenosis exhibiting myocardial hypertrophy but still preserved cardiac function (see Methods in the online-only Data Supplement) showed an increase in CaMKIIδ expression compared with samples from control hearts that were not hypertrophied (+24.7±9.7%; Figure 4C and 4D).

Gene Array Analysis

To further define the molecular signature of the 2 load models, we performed genome-wide expression profiling.

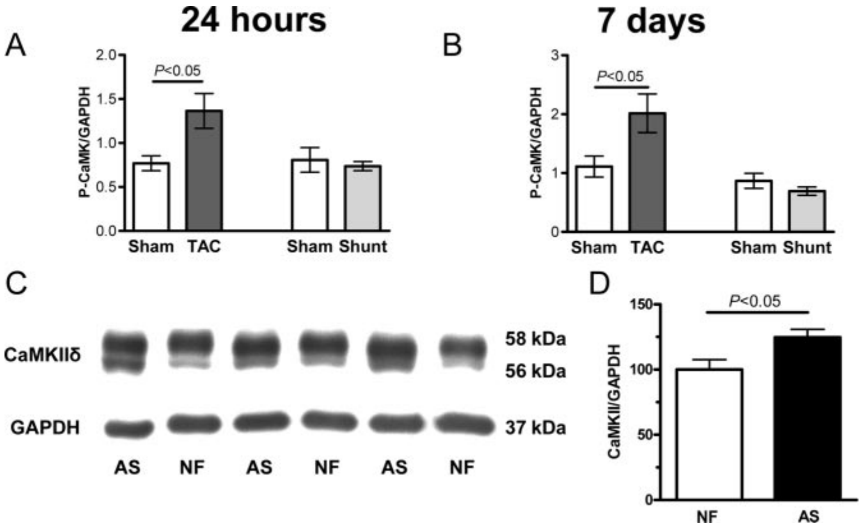

Figure 4. Activation of signaling pathways in sham, TAC, and shunt animals 24 hours and 7 days after intervention (n=6 per group). A and B, Phosphorylated CaMK normalized to GAPDH (A, 24 hours; B, 7 days after intervention). C and D, CaMK expression normalized to GAPDH in human nonfailing (NF) versus aortic stenosis (AS) samples (n=6 per group).

Applying a moderated linear model and the false discovery rate method for multiple testing with a threshold of 5% resulted in 1399 (1954 probes sets) upregulated and 1513 (1896 probes sets) downregulated annotated genes in the TAC compared with the sham group. In the shunt group compared with sham, 315 (384 probes sets) upregulated and 704 (853 probes sets) downregulated annotated genes were identified (Figure 5A and 5B and Tables I and II in the online-only Data Supplement). Comparing the differences between TAC and shunt groups directly (up or down) resulted in 157 differentially expressed genes (187 probes sets; Table III in the online-only Data Supplement). Unsupervised hierarchical clustering of these 157 genes (187 probes sets) resulted in accurate identification of the cardiac gene expression profiles of individual animals in the appropriate groups (Figure VII in the online-only Data Supplement). Of the candidate genes identified by the aforementioned protein analysis, an increased expression of CaMKIIδ was selectively found in the TAC but not in the shunt group. Of the 157 differentially expressed genes, 122 were regulated only in TAC, 21 were regulated only in shunt, and 14 were significantly regulated in both models. Of the 14 genes, 6 were regulated in parallel but at a different amount and 8 in an opposite direction (brain-derived neurotrophic factor; protein phosphatase 1B, magnesium dependent, beta isoform; c-myc binding protein; RIKEN complementary DNA 1190002N15 gene; phosphodiesterase 4D interacting protein [myomegalin]; serine/threonine kinase 38 like; amine oxidase, copper-containing 3; B and T lymphocyte associated).

Furthermore, pathway analysis revealed 90 pathways selectively regulated in the TAC group, 10 pathways similarly regulated in the TAC and shunt groups, and 4 pathways selectively regulated in the shunt group (Tables IV and V in the online-only Data Supplement). We confirmed cardiomyocyte apoptosis, inflammation, increased cell cycle activity, and fibrosis in the pathway analysis confined to the TAC model. Among the selectively regulated pathways in the shunt model, activation of the Wnt signaling is of special interest (Table 3).

Load-Dependent Regulation of MicroRNAs

The expression of microRNAs was evaluated in both models. At 24 hours, none of the microRNAs assayed by microarray exhibited differential expression between the experimental groups (data not shown). After 7 days of subjection to load, we identified 13 microRNAs differentially regulated between TAC and shunt groups. Of these, 9 were selectively regulated in the TAC model, 3 were selectively regulated in the shunt model, and 1 was regulated in parallel but at significantly different amounts in both models (Figure 5C through 5E).

Single Cell Function

Seven days after intervention, increased cardiomyocyte fractional shortening (+24%; $P<0.05$) and intracellular calcium transients (+13%; $P<0.05$) were seen at a 1-Hz stimulation rate in TAC mice (Figure 6A, 6B, 6E, and 6F). Sarcoplasmic reticulum (SR) calcium load was unchanged, whereas fractional SR calcium release was significantly increased in TAC mice by 27% (Figure 6G and 6H). In contrast, in cardiomyocytes from shunt mice, fractional shortening and calcium cycling were not different from those of sham mice (Figure 6C through 6H).

Mechanisms underlying the observed alteration in calcium cycling in TAC mice were studied in detail. The increase in SR calcium fractional release was clearly CaMKII dependent because KN-93, a CaMKII inhibitor, normalizes SR calcium fractional release (Figure 7A). The enhancement of fractional SR calcium release in TAC mice could be due to increased L-type calcium current or increased ryanodine receptor sensitivity, both regulated by CaMKII.[9] Calcium spark frequency as an estimate of ryanodine receptor sensitivity was largely increased in TAC mice (+206%, $P<0.001$; Figure 7B and 7C). Measurement of action potentials as an indicator of calcium influx showed a prolongation of the action potential duration (APD_{90}) in TAC compared with sham mice ($P<0.001$; Figure 7D and 7E). This prolongation could be abolished by CaMKII inhibition with autocamtide-2 related inhibitory peptide ($P<0.001$) or L-type calcium channel inhibition with nifedipine ($P<0.001$; Figure 7D and 7E). Furthermore, direct measurement of L-type calcium current showed a significant increase in TAC versus sham mice ($P<0.05$), which could be normalized by addition of the CaMKII inhibitor autocamtide-2 related inhibitory peptide ($P<0.05$; Figure 7F and 7G). This indicates that increased

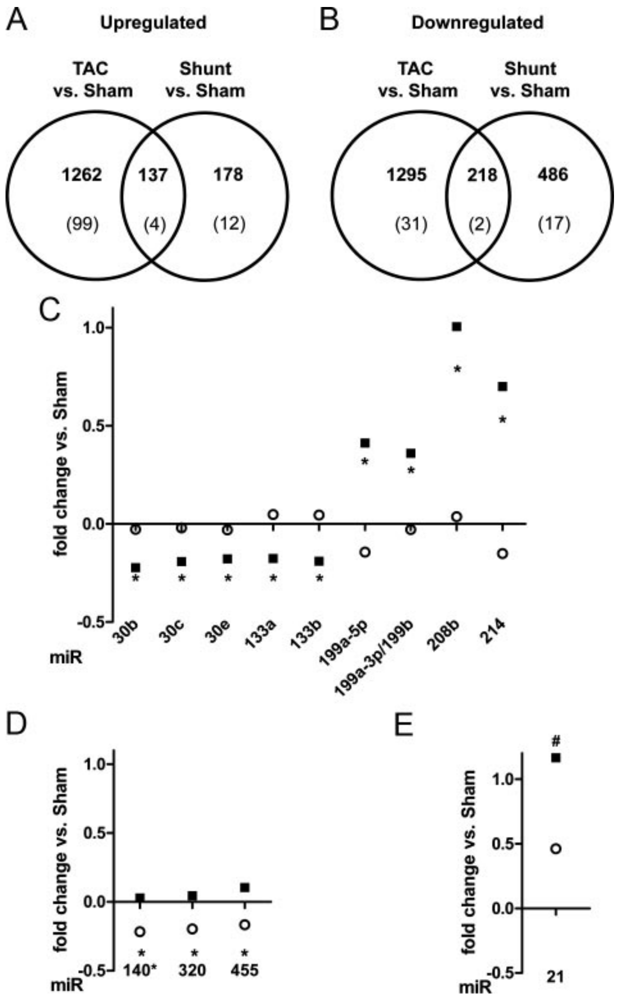

Figure 5. Analysis of gene and microRNA expression by microarrays 7 days after intervention. A and B, Number of differentially expressed genes in TAC and shunt (n=4 per group). Lower numbers indicate the number of genes with a significant regulation between TAC and sham or shunt and sham as well as between TAC and shunt models. A, Upregulated genes. B, Downregulated genes. C through E, Analysis of microRNA expression by microarrays (n=5 per group) after 7 days in TAC (■) and shunt groups (○). Only microRNAs with a significantly different expression between TAC and shunt are shown (TAC vs shunt,**P*<0.01, # *P*<0.02). C, MicroRNAs significantly regulated in TAC vs sham (*P*<0.01). D, MicroRNAs significantly regulated in shunt vs sham (*P*<0.01). E, MicroRNAs significantly regulated in TAC and shunt vs the corresponding sham (*P*<0.01).

L-type calcium current is the primary mechanism of the APD prolongation and suggests that increased fractional release results from both increased L-type current and increased ryanodine receptor sensitivity.

Analysis of CaMKIIδ-Knockout Mice

To better understand the role of CaMKII activation in pressure-overload hypertrophy, we used the CaMKIIδ-knockout mouse model.[10] One week after TAC, the amount of perivascular fibrosis was similarly increased in wild-type and knockout mice (Figure 8A and 8B). However, the amount of cardiomyocyte apoptosis after TAC was significantly lower in the knockout compared with the wild-type hearts (*P*<0.01; Figure 8C).

Table 3. Gene Array Findings of Special Interest

ID	Name	TAC	Shunt
1433761_at	Phosphodiesterase 4D interacting protein (myomegalin)	↑	↓
1439168_at	CaMKIIδ	↑	NS
X04310	Wnt signaling pathway	NS	↑
Inflammation			
04650	Natural killer cell–mediated cytotoxicity	↑	NS
X04660	T-cell receptor signaling pathway	↑	NS
X04662	B-cell receptor signaling pathway	↑	NS
X04670	Leukocyte transendothelial migration	↑	NS
Cell cycle activity			
X03030	DNA replication	↑	NS
X04110	Cell cycle	↑	NS
Apoptosis			
X04210	Apoptosis	↑	NS
X04115	p53 signaling pathway	↑	NS
Fibrosis			
X04512	Extracellular matrix receptor interaction	↑	NS
X04514	Cell adhesion molecules	↑	NS

Selected findings from the gene array are shown. Total results are shown in Tables I through V in the online-only Data Supplement. NS indicates not significant.

Discussion

The present study shows that with a comparable elevation of wall stress myocardial structure, largely different molecular phenotypes develop with preload versus afterload, although the extent of cardiac hypertrophy is similar. (1) Increased afterload with TAC resulted in increased BNP expression, which was not seen by increased preload in the shunt model during the first 7 days. (2) TAC resulted in concentric hypertrophy with increased fibrosis, inflammation, and cardiomyocyte apoptosis, whereas eccentric hypertrophy in the shunt model occurred without increased fibrosis, without inflammation, and with less cardiomyocyte apoptosis. (3) TAC hypertrophy resulted in development of severe left ventricular dysfunction and higher mortality compared with shunt hypertrophy. (4) Signaling analysis showed that the hypertrophic phenotype in TAC was associated with persistent activation of CaMKII and disturbed intracellular calcium cycling. None of these changes happened in the shunt model, in which Akt was persistently activated. (5) CaMKIIδ-knockout mice and pharmacological CaMKII inhibition led to normalization of disturbed calcium cycling and a reduced rate of cardiomyocyte apoptosis. We conclude that afterload results in disturbed calcium cycling and CaMKII activation and maladaptive hypertrophy, whereas preload results in a more favorable type of hypertrophy through stretch-mediated activation of Akt.

Load and neurohormones regulate the function and phenotypic characteristics of the myocardium. Afterload results in a concentric hypertrophic phenotype that was often viewed as

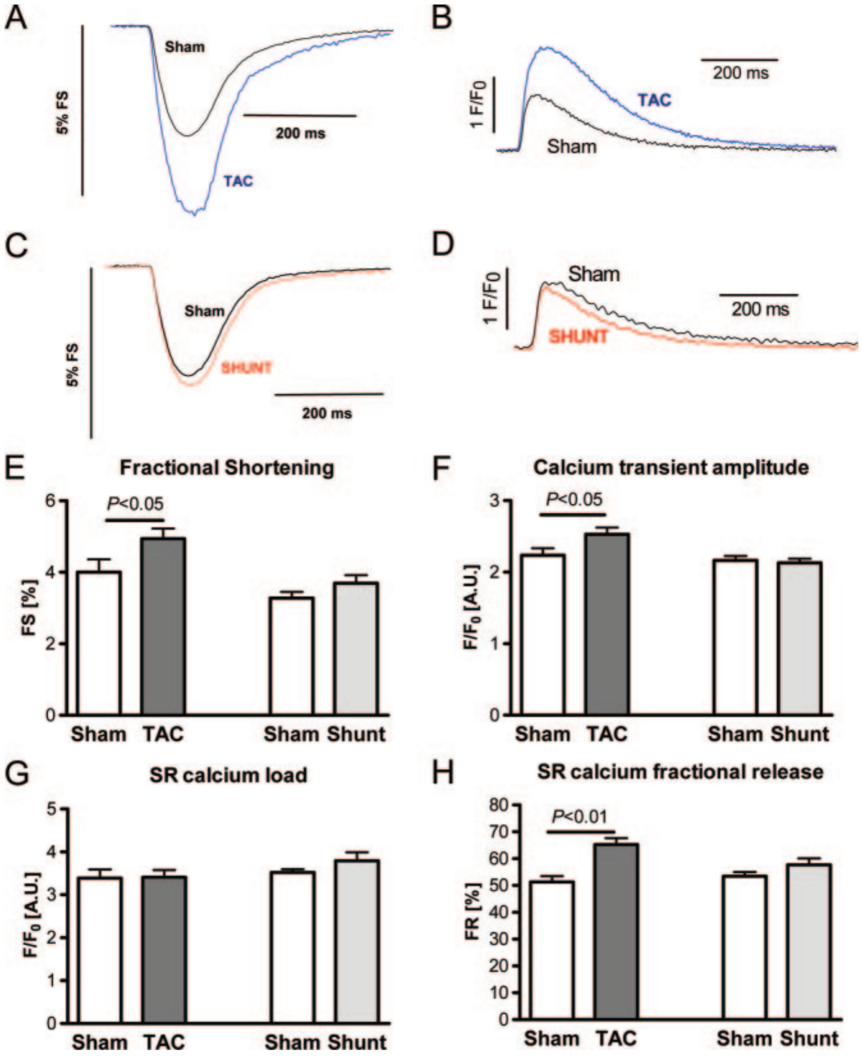

Figure 6. Single cell function in sham, TAC, and shunt groups 7 days after intervention. A and C, Example of fractional shortening (FS) of cardiomyocytes from TAC (A) and shunt (C) animals compared with sham. B and D, Example of calcium transients of cardiomyocytes from TAC (B) and shunt (D) animals compared with sham. E, Fractional shortening (number of cells: 36/44/59/55). F, Calcium transient amplitude (F/F_0) (number of cells: 36/44/59/55). G, SR-calcium content measured by caffeine application (number of cells: 29/36/39/24). H, Fractional SR calcium release measured as calcium transient per SR calcium load (number of cells: 28/32/39/24). FR indicates fractional release.

compensatory in nature because increased wall thickness reduces wall stress according to the law of Laplace. Preload results in eccentric hypertrophy. Although earlier studies suggested that volume overload with uncompensated wall stress would be disadvantageous, more recent studies suggested that volume overload was associated with a more favorable remodeling compared with pressure overload.[11,12] The present study shows that with identical wall stress myocardial structure, cardiac function and mortality are more favorable with the shunt model than with the TAC model. This suggests that elevation of wall stress by itself may not be a critical issue. Indeed, genetically modified mice with improved cardiac function and prognosis after TAC exhibited modified protein expression but absence of hypertrophic response.[13] Thus, the composition of the myocardium in response to increased load by compensation on a molecular level may be more relevant than the degree of hypertrophy (ie, wall thickness).

We studied signaling at 24 hours, assuming that at this early time point load-mediated activation of signaling cascades and gene expression dominates over secondary effects such as neurohumoral activation, and we studied signaling at 7 days to identify those signals being consistently activated by load. The maladaptive phenotype in TAC can be partially attributed to CaMKII signaling, which is functionally associated with defective calcium cycling. Wang et al[14,15] suggested previously that afterload activates L-type calcium current. The present study indicates that increased L-type calcium current predominantly results from CaMKII activation because it can be reversed with CaMKII inhibition. Furthermore, CaMKIIδ activation induces cardiomyocyte apoptosis in TAC, as indicated by the reduced rate of cardiomyocyte apoptosis in the CaMKIIδ-knockout animals. This confirms in vivo the recent suggestions in an in vitro study showing that CaMKII inhibition prevented cardiomyocyte apoptosis after angiotensin II exposure of rat and mouse cardiomyocytes.[16] Furthermore, the mechanistic relevance of CaMKII-dependent cardiomyocyte apoptosis for the development of the maladaptive hypertrophic phenotype is supported by previous data showing that in CaMKIIδ-knockout mice, progression to heart failure is reduced after TAC.[17] Interestingly, in a previous study we showed reduced interstitial fibrosis in TAC in CaMKIIδ-knockout mice at 3 weeks.[10] This previous work also showed that CaMKIIδ-knockout does not result in upregulation of other CaMK isoforms. This suggests that increased cardiomyocyte apoptosis may be a major component of CaMKII-mediated maladaptive hypertrophy during increased afterload. Interstitial fibrosis at later stages may reflect

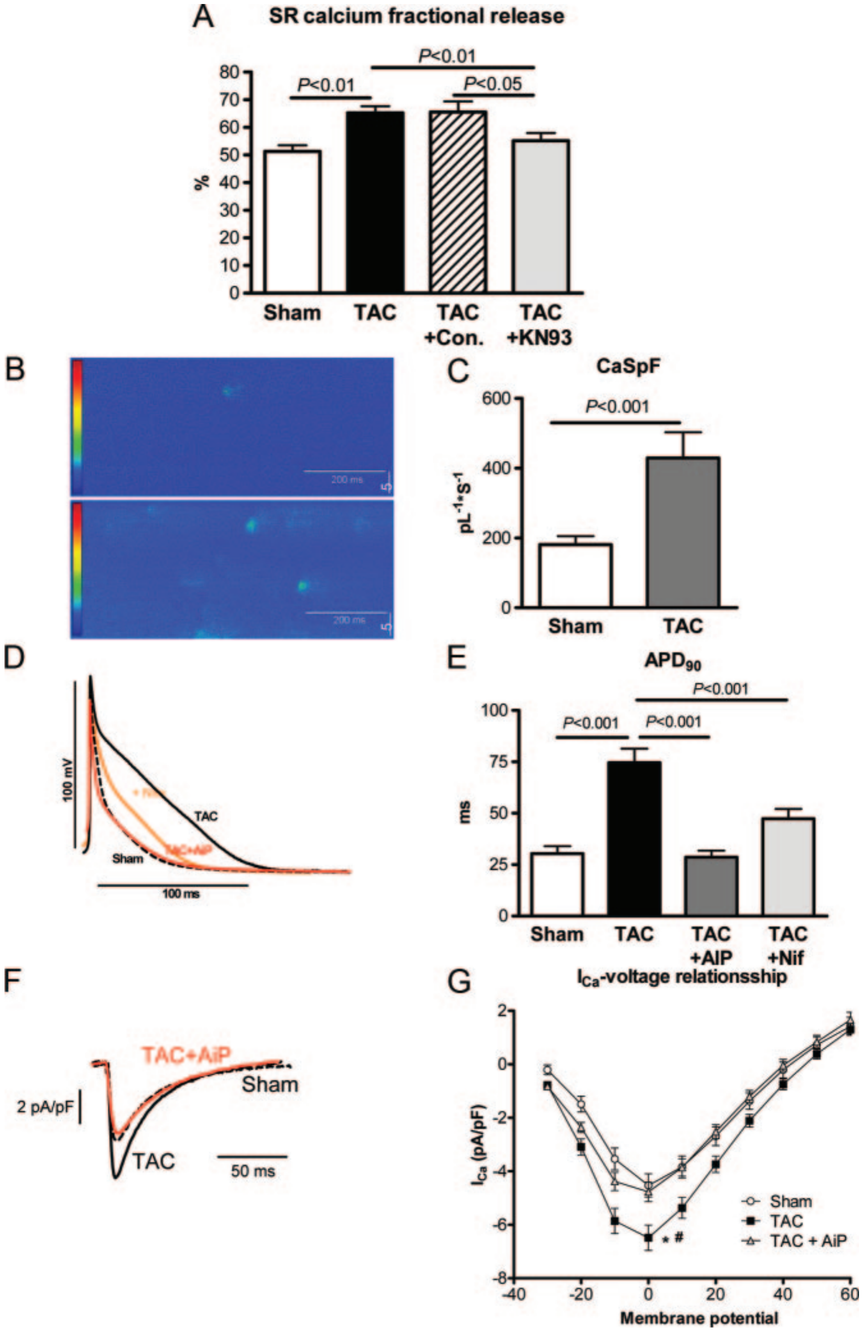

Figure 7. Role of CaMK in TAC-induced calcium cycling alteration 7 days after intervention. A, Fractional SR calcium release in sham, TAC, TAC plus control (Con.) (KN92), and TAC plus KN93 (CaMK inhibitor) (number of cells: 28/32/14/16). B, Example of calcium spark measurement in sham and TAC. C, Ca^{2+} spark frequency (CaSpF) in sham and TAC (number of cells: 17/20). D, Original recordings of action potential measurements in sham (dotted line), TAC (black line), TAC plus AiP (CaMKII inhibition; red line), and TAC+ plus nifedipine (Nif) (orange line). Aip indicates Autocamtide-2 Related Inhibitory Peptide. E, APD (APD_{90}) in sham, TAC, TAC plus AiP (CaMKII inhibition), and TAC plus nifedipine (number of cells: 16/52/10/16). F, Original recordings of L-type Ca^{2+} current in sham, TAC, and TAC plus AiP (CaMKII inhibition) at 0 mV. G, L-type Ca^{2+} current in sham, TAC, and TAC plus AiP (number of cells: 11/13/16; *$P<0.05$ in sham vs TAC; #$P<0.05$ in TAC vs TAC plus AiP).

replacement fibrosis after cardiomyocyte apoptosis. However, these data also suggest that early perivascular fibrosis (1 week) occurs independently from CaMKII activity and is possibly related to inflammation.

In shunt-induced preload elevation, calcium cycling is normal, and none of the afterload-related signals are activated. In contrast, Akt is activated, which is generally believed to promote a more adaptive hypertrophic phenotype.[18] One may speculate that Akt could be activated by a preload-mediated stretch of titin or related proteins involved in the sensing of preload.

Interestingly, ventricular BNP expression occurs only with increased afterload and not with elevated preload. This supports for the first time in vivo the suggestions from previous in vitro studies.[7,8] BNP may prevent more pronounced hypertrophy in TAC.

Gene array analysis shows a largely different gene expression pattern between TAC and shunt models. Interestingly, 8 genes were significantly regulated in the opposite direction in both models. Among these, the phosphodiesterase 4D interacting protein (myomegalin) is upregulated in the TAC and downregulated in the shunt model. Myomegalin is localized in the Z-disc,[19] interacts with the phosphodiesterase 4D, and is also involved in regulation of stress-dependent nuclear trafficking of myopodin.[20] Furthermore, gene array pathway analysis confirms an activation of inflammation, fibrosis, and cardiomyocyte apoptosis pathways in the TAC model (Table 3), whereas in the shunt model, selective activation of the Wnt pathway is an interesting finding. The Wnt pathway may influence eccentric hypertrophy via Akt, which was shown here to be consistently activated by phospho-protein analysis.[21]

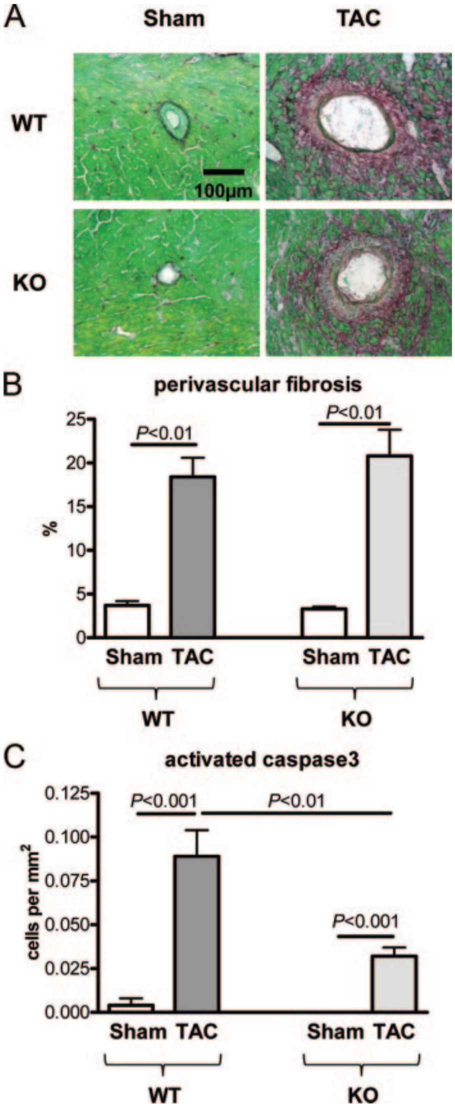

Figure 8. Role of CaMKIIδ-knockout (KO) in TAC-induced hypertrophy (n=5 per group) 7 days after intervention. A, Histological sections stained for fibrosis (Sirius red). B, Statistical analysis of perivascular fibrosis. C, Rate of cardiomyocyte apoptosis by activated caspase3 staining. WT indicates wild-type.

MicroRNAs control expression of gene clusters. MicroRNA array analysis also identifies significant differences between both load models. These include absence of regulation of microRNAs 133, 30, and 208 in the shunt model, which are regulated in TAC and associated with hypertrophy and fibrosis.[22–24] Furthermore, microRNA 208 expression is necessary for ß-MHC upregulation after TAC.[23] Here microRNA 208b upregulation is paralleled by ß-MHC upregulation. MicroRNA 140*, 320, and 455 are regulated in shunt but not in TAC models. MicroRNA 140* and 320 have been described as upregulated in TAC[22] or human heart failure,[25] and upregulation of microRNA 320 is associated with apoptosis.[26] MicroRNA 455 has not been described previously to be regulated in the heart. Interestingly, microRNA regulation was not observed after 24 hours following surgery. This may suggest that microRNAs regulate later changes in gene expression during overload. Differentially regulated genes in TAC and shunt models support qualitative differences in both load forms and eliminate concerns that preload is just a milder stress than afterload. The mechanistic relevance of newly identified genes and pathways in load-dependent cardiac hypertrophy is hypotheses generating and warrants further studies with differential consideration of preload and afterload.

Pathophysiological and Therapeutic Implications

TAC is associated with inflammation, fibrosis, and cardiomyocyte apoptosis, which may impair myocardial function directly. Moreover, fibrosis may critically increase the diffusion distance of oxygen to myocytes and thereby influence cardiac energetics and function.[27] In the shunt group, no inflammation and fibrosis were observed. A small level of apoptosis may be the mechanism underlying late decline of cardiac function.[28] The present data also suggest that increased load may require differential pharmacological interventions depending on the contribution of preload and afterload. With increased afterload such as occurs in arterial hypertension or aortic stenosis, strategies to inhibit CaMKII signaling may be beneficial by reducing cardiomyocyte apoptosis. In diseases associated with increased preload predominantly, such as mitral regurgitation or aortic regurgitation, CaMKII inhibition would not be a rational approach to treat this type of hypertrophy.

The present findings may also be relevant for the design of experimental studies. Many studies use the TAC model in genetically modified mice to study the influence of genes on increased load. One should now consider that the shunt model may provide additional information.[29,30] Furthermore, load experiments in isolated cardiomyocytes are frequently performed by flex membrane stretching of cells. Under those circumstances, it should be taken into account that stretch of cardiomyocytes may have completely different effects depending on its occurrence in diastole, where it elevates preload, or in systole, where it elevates afterload.

Acknowledgments

We are grateful to Brigitte Korff and Thomas Sowa for excellent technical assistance.

Sources of Funding

This work was supported by the Deutsche Forschungsgemeinschaft (grant Klinische Forschergruppe 155: TP1,3,4,5,7,8 [KO 1872/2–1 to Dr Hasenfuss; SE 1117/1–1 to Dr Seidler; LE 1313/2–1 to Dr Lehnart; MA 1982/2–2 to Dr Maier; EN 84/21–1 to Dr Schäfer; LI 690/7–2 to Dr Linke]), National Institutes of Health grant HL085098 (to Dr Field), Emmy-Noether Program (BA2258–2-1 to Dr Backs), and EUGeneHeart (project No. LSHM-CT-2005–018833). Dr Maier is also funded by a DFG-Heisenberg grant (MA 1982/4–1) and the Fondation Leducq Award to the Alliance for Calmodulin-Kinase Signaling in Heart Disease.

Disclosures

None.

References

1. Grossman W, Jones D, McLaurin LP. Wall stress and patterns of hypertrophy in the human left ventricle. *J Clin Invest*. 1975;56:56–64.
2. Frank D, Kuhn C, Katus HA, Frey N. The sarcomeric Z-disc: a nodal point in signalling and disease. *J Mol Med*. 2006;84:446–468.
3. Linke WA. Sense and stretchability: the role of titin and titin-associated proteins in myocardial stress-sensing and mechanical dysfunction. *Cardiovasc Res*. 2008;77:637–648.

4. von Lewinski D, Stumme B, Fialka F, Luers C, Pieske B. Functional relevance of the stretch-dependent slow force response in failing human myocardium. *Circ Res*. 2004;94:1392–1398.
5. Norton JM. Toward consistent definitions for preload and afterload. *Adv Physiol Educ*. 2001;25:53–61.
6. Buitrago M, Lorenz K, Maass AH, Oberdorf-Maass S, Keller U, Schmitteckert EM, Ivashchenko Y, Lohse MJ, Engelhardt S. The transcriptional repressor Nab1 is a specific regulator of pathological cardiac hypertrophy. *Nat Med*. 2005;11:837–844.
7. Kögler H, Schott P, Toischer K, Milting H, Nguyen van P, Kohlhaas M, Grebe C, Kassner A, Domeier E, Teucher N, Seidler T, Knöll R, Maier LS, El-Banayosy A, Körfer R, Hasenfuss G. Relevance of brain natriuretic peptide in preload-dependent regulation of cardiac sarcoplasmic reticulum Ca^{2+} ATPase expression. *Circulation*. 2006;113:2724–2732.
8. Toischer K, Kögler H, Tenderich G, Grebe C, Seidler T, Nguyen Van P, Jung K, Knöll R, Körfer R, Hasenfuss G. Elevated afterload, neuroendocrine stimulation, and human heart failure increase BNP levels and inhibit preload-dependent SERCA upregulation. *Circ Heart Fail*. 2008; 1:265–271.
9. Maier LS, Bers DM. Role of Ca^{2+}/calmodulin-dependent protein kinase (CaMK) in excitation-contraction coupling in the heart. *Cardiovasc Res*. 2007;73:631–640.
10. Backs J, Backs T, Neef S, Kreusser MM, Lehmann LH, Patrick DM, Grueter CE, Qi X, Richardson JA, Hill JA, Katus HA, Bassel-Duby R, Maier LS, Olson EN. The delta isoform of CaM kinase II is required for pathological cardiac hypertrophy and remodeling after pressure overload. *Proc Natl Acad Sci U S A*. 2009;106:2342–2347.
11. Opie LH, Commerford PJ, Gersh BJ, Pfeffer MA. Controversies in ventricular remodelling. *Lancet*. 2006;367:356–367.
12. Linzbach AJ. Heart failure from the point of view of quantitative anatomy. *Am J Cardiol*. 1960;5:370–382.
13. Hill JA, Karimi M, Kutschke W, Davisson RL, Zimmerman K, Wang Z, Kerber RE, Weiss RM. Cardiac hypertrophy is not a required compensatory response to short-term pressure overload. *Circulation*. 2000;101: 2863–2869.
14. Wang Y, Tandan S, Cheng J, Yang C, Nguyen L, Sugianto J, Johnstone JL, Sun Y, Hill JA. Ca^{2+}/calmodulin-dependent protein kinase II-dependent remodeling of Ca^{2+} current in pressure overload heart failure. *J Biol Chem*. 2008;283:25524–25532.
15. Wang Z, Kutschke W, Richardson KE, Karimi M, Hill JA. Electrical remodeling in pressure-overload cardiac hypertrophy: role of calcineurin. *Circulation*. 2001;104:1657–1663.
16. Palomeque J, Rueda OV, Sapia L, Valverde CA, Salas M, Petroff MV, Mattiazzi A. Angiotensin II–induced oxidative stress resets the Ca^{2+} dependence of Ca^{2+}-calmodulin protein kinase II and promotes a death pathway conserved across different species. *Circ Res*. 2009;105: 1204–1212.
17. Ling H, Zhang T, Pereira L, Means CK, Cheng H, Gu Y, Dalton ND, Peterson KL, Chen J, Bers D, Heller Brown J. Requirement for Ca^{2+}/calmodulin-dependent kinase II in the transition from pressure overload-induced cardiac hypertrophy to heart failure in mice. *J Clin Invest*. 2009;119:1082–1085.
18. Shiojima I, Walsh K. Regulation of cardiac growth and coronary angiogenesis by the Akt/PKB signaling pathway. *Genes Dev*. 2006;20: 3347–3365.
19. Verde I, Pahlke G, Salanova M, Zhang G, Wang S, Coletti D, Onuffer J, Jin SL, Conti M. Myomegalin is a novel protein of the golgi/centrosome that interacts with a cyclic nucleotide phosphodiesterase. *J Biol Chem*. 2001;276:11189–11198.
20. Faul C, Dhume A, Schecter AD, Mundel P. Protein kinase A, Ca2+/calmodulin-dependent kinase II, and calcineurin regulate the intracellular trafficking of myopodin between the Z-disc and the nucleus of cardiac myocytes. *Mol Cell Biol*. 2007;27:8215–8227.
21. Blankesteijn WM, van de Schans VA, ter Horst P, Smits JF. The Wnt/frizzled/GSK-3 beta pathway: a novel therapeutic target for cardiac hypertrophy. *Trends Pharmacol Sci*. 2008;29:175–180.
22. Sayed D, Hong C, Chen IY, Lypowy J, Abdellatif M. MicroRNAs play an essential role in the development of cardiac hypertrophy. *Circ Res*. 2007;100:416–424.
23. van Rooij E, Sutherland LB, Qi X, Richardson JA, Hill J, Olson EN. Control of stress-dependent cardiac growth and gene expression by a microRNA. *Science*. 2007;316:575–579.
24. Carè A, Catalucci D, Felicetti F, Bonci D, Addario A, Gallo P, Bang ML, Segnalini P, Gu Y, Dalton ND, Elia L, Latronico MV, Høydal M, Autore C, Russo MA, Dorn GW II, Ellingsen O, Ruiz-Lozano P, Peterson KL, Croce CM, Peschle C, Condorelli G. MicroRNA-133 controls cardiac hypertrophy. *Nat Med*. 2007;13:613–618.
25. Thum T, Galuppo P, Wolf C, Fiedler J, Kneitz S, van Laake LW, Doevendans PA, Mummery CL, Borlak J, Haverich A, Gross C, Engelhardt S, Ertl G, Bauersachs J. MicroRNAs in the human heart: a clue to fetal gene reprogramming in heart failure. *Circulation*. 2007;116: 258–267.
26. Ren XP, Wu J, Wang X, Sartor MA, Qian J, Jones K, Nicolaou P, Pritchard TJ, Fan GC. MicroRNA-320 is involved in the regulation of cardiac ischemia/reperfusion injury by targeting heat-shock protein 20. *Circulation*. 2009;119:2357–2366.
27. Kai H, Kuwahara F, Tokuda K, Imaizumi T. Diastolic dysfunction in hypertensive hearts: roles of perivascular inflammation and reactive myocardial fibrosis. *Hypertens Res*. 2005;28:483–490.
28. Dent MR, Das S, Dhalla NS. Alterations in both death and survival signals for apoptosis in heart failure due to volume overload. *J Mol Cell Cardiol*. 2007;43:726–732.
29. Chaturvedi RR, Herron T, Simmons R, Shore D, Kumar P, Sethia B, Chua F, Vassiliadis E, Kentish JC. Passive stiffness of myocardium from congenital heart disease and implications for diastole. *Circulation*. 2010; 121:979–988.
30. Zheng J, Chen Y, Pat B, Dell'italia LA, Tillson M, Dillon AR, Powell PC, Shi K, Shah N, Denney T, Husain A, Dell'Italia LJ. Microarray identifies extensive downregulation of noncollagen extracellular matrix and profibrotic growth factor genes in chronic isolated mitral regurgitation in the dog. *Circulation*. 2009;119:2086–2095.

CLINICAL PERSPECTIVE

Hemodynamic load regulates myocardial function and gene expression. Increased load triggers molecular, structural, and functional remodeling and eventually heart failure. Increased left ventricular load acts either as preload because of left to right shunt or aortic or mitral regurgitation or as increased afterload because of aortic stenosis or arterial hypertension. In the present study, different cardiac gene expression, signaling, and remodeling with preload or afterload were studied in mice with aortocaval shunt (preload) or transverse aortic constriction (afterload) with matched mean total wall stresses. Here we show that increased afterload results in maladaptive hypertrophy with increased fibrosis, inflammation, cardiomyocyte apoptosis, development of heart failure, and increased mortality. Increased preload results in a more favorable type of hypertrophy without increased fibrosis and inflammation and with less apoptosis and better survival. Ventricular brain natriuretic peptide expression is increased only with afterload but not with preload. Gene expression and signaling pathways differ considerably with preload and afterload. Calcium/calmodulin-dependent protein kinase IIδ–mediated signaling may be the dominant maladaptive pathway in pressure overload, whereas activation of the Akt pathway may be dominant in volume overload. The data indicate that differential therapeutic strategies should be developed to address the specific signaling pathways activated with preload versus afterload. This may prevent or delay the development of heart failure in patients with increased preload or afterload, respectively.

SUPPLEMENTAL MATERIAL

Differential cardiac remodeling in preload versus afterload

	Page:
Expanded material and methods	**2-13**
Supplementary Figure:	**14-20**
Figure Legend:	**21-22**
References	**23-25**

Gene-Array analysis:

Table I

Genes upregulated in TAC	**26-66**
Genes downregulated in TAC	**67-107**

Table II

Genes upregulated in Shunt	**108-116**
Genes downregulated in Shunt	**117-135**

Table III

Genes significantly regulated between both models and

Regulated compared to both sham	**136**
Regulated only in TAC	**137-140**
Regulated only in Shunt	**141**

Table IV

Signal pathways activated in TAC	**142**
Signal pathways repressed in TAC	**143**

Table V

Signal pathways activated in Shunt	**145**
Signal pathways repressed in Shunt	**145**

EXPANDED MATERIAL AND METHODS

Animals

The investigation conforms to the *Guide for the Care and Use of Laboratory Animals* (NIH publication No. 85–23, revised 1996). For the present study following only female animals were used.

Aortocaval shunt operation (Shunt)

Surgery was done as described previously.[1] Briefly, 12 week old female FVBN mice were anesthetized using isolfluran insufflation. A longitudinal abdominal incision was made and the vessels prepared. The aorta was clamped and punctured with a needle (23G) through the vena cava inferior. After removing the needle the external hole in the aorta was closed by a cyanoacrylate glue (Pattex, Düsseldorf, Germany). In successful shunt operations mixing of oxygenated blood from the abdominal aorta in the vena cava could be observed. The abdomen was then closed and the mice were kept on a heating plate until full recovery from anesthesia. Sham animals underwent the same procedure except for the puncture of the vessels. At the end of the experiments mice were intubated, ventilated with 100% O2 and Isofluran. Blood was drawn from the right ventricle and O2 saturation was measured. Only animals with an right ventricular O2 saturation over 90% were analyzed.

Transverse aortic constriction (TAC)

Surgery was done using a minimally invasive approach as described previously.[2] Briefly, 12 weeks old female FVBN mice were anesthetized using intraperitoneal injections of ketamine and xylazine (100mg/kg + 5mg/kg). A horizontal incision at the jugulum was used to display the transversal aorta. A 27 gauge needle was tied against the aorta using a 5-0 non-absorbable suture. After removal of the 27 gauge needle, skin was closed and the mice were kept on a heating plate until recovering from anesthesia. Sham animals underwent the same procedure except banding of the transversal aorta. At the end of the experiment mice were euthanized by isofluran insufflation.

Echocardiography

2D guided M-mode echocardiography was performed using a VS-VEVO 660/230 High Resolution Imaging System (Visualsonics, Toronto, Canada). Mice were lightly anesthetized with 2.5% 2-2-2 Tribromoethanol (avertin, 0.01 ml/g i.p.) and were allowed to breathe spontaneously. LV end-diastolic (LVEDD) and end-systolic (LVESD) dimensions were measured from original tracings by using the leading edge convention of the American Society of Echocardiography. LV percent fractional shortening (FS), LV mass (LVM) were calculated as previously described.[3]

In-vivo hemodynamic measurements

Cardiac catheter and pressure-volume messurements.[4] Mice were anesthetized by isoflurane inhalation and intubated. Anesthesia was maintained by continuous isoflurane inhalation (1.5% vol.). The mice were ventilated with a volume-controlled ventilator (Minivent, Harvard Apparatus, Holliston, MA, USA) with a tidal volume of 150 µl and a frequency of 150 breaths/minute. The end-exspiratory pressure (PEEP) was kept constant at 1 cm H2O by immersion of the exspiration tube into water. Body temperature was measured with a rectal probe and kept constant at 37°C by a heating pad and an infrared bulb with feedback regulation (TKM-0903, FMI GmbH, Seeheim, Germany). The right carotid artery was accessed via a mid-cervical incision. After distal ligation and proximal clamping the artery was cut open and the catheter was inserted. After releasing the proximal clamp the catheter was secured by a ligation around the artery and advanced into the left ventricle. To assure adequate preload, fluid supplementation was provided by intraperitoneal injection of physiological saline (30ml/kg). Baseline hemodynamic parameters were measured at least 10 min after saline injection when a stable reading of pressure and volume was obtained. After the hemodynamic measurements the offset of the volume signal (parallel volume, VP) was determined by injection of 10 µl hypertonic saline (5%) via a 30G catheter into the left jugular vein. At the end of the experiment the catheter was withdrawn from the carotid artery, the mouse was killed by cervical dislocation and the blood was sampled in a heparinized syringe for determination of the blood conductance by use of the cuvettes provided by the manufacturer.

Histological analyses

Tissues were harvested and processed for cryo sectioning using standard techniques[5]. Activated caspase-3 immune reactivity (antibody #G7481, Promega, Madison, WI) was performed on post-fixed sections (horseradish peroxidase-conjugated secondary antibody, diaminobenzidine reaction) as described previously[6]. Sirius red-Fast green staining was performed and quantitated on sections post-fixed in Bouin's solution as described previously.[7,8] To quantitate atrial collagen content, images were captured with a digital camera and the red pixel content of the myocardium was measured using Adobe Photoshop 5.5 and Scion Images for Windows Beta 4.0.2 software. Minimal cardiomyocyte fiber diameter was calculated as described.[9,10] At least 400 randomly selected cardiomyocytes from each animal were analyzed. TUNEL analysis were performed on adjacent sections using the ApopTag Apoptosis Detection kit according to the manufacturer's procedures (Chemicon International, Billerica, MA). Monoclonal rat anti-mouse antibodies against CD45 were used to detect leucocytes (clone 30-F11; sc-53665; abcam; dilution, 1:75). After incubation overnight at 4°C or 1 hour at RT, respectively, and subsequent washing in PBS, PE-labeled secondary goat anti-rat antibodies (dilution, 1:400; Molecular Probes) were added for 60 minutes. Cell nuclei were visualized using diamidino-4',6'-phenyl-2-indoledichlorhydrate

(DAPI; Sigma; dilution, 1:200), mounted in VectaShield (Vector) and inspected on a Zeiss axiovert fluorescence microscope. The number of CD45-positive leucocytes was evaluated on 6 randomly selected microscope fields (400x magnification) and expressed per mm² (for CD45).

Measurement of DNA synthesis

DNA synthesis was monitored using a tritiated thymidine incorporation assay (200 µCi I.P. at 28 Ci/mM, Amersham, Arlington Heights, IL) in combination with the MHC-nLAC reporter transgenic strain.[9,11]. Mice were injected with thymidine 1 weeks following surgery (TAC, Shunt or the respective sham surgeries). Standard methods were employed for cryosectioning[8] Beta-galactosidase activity was detected by staining with 5-bromo-4-chloro-3-indolyl-beta-D-galactoside (X-GAL), and autoradiography was performed as described.[11] The presence of silvergrains over blue nuclei (i.e., X-GAL stained nuclei) was indicative of cardiomyocyte DNA synthesis, while the presence of silvergrains over Hoechst-stained nuclei was indicative of non-myocyte DNA synthesis.

Isolation of cardiomyocytes and measurement of cell length

Cardiac myocyte isolation was performed as described previously.[12] In brief, mice were anesthetized with isoflurane, hearts were excised and mounted on a Langendorff perfusion-system and retrogradely perfused with a nominally Ca-free Tyrodes' solution containing (in mM) NaCl 113, KCl 4.7, KH_2PO_4 0.6, $Na_2HPO_4x2H_2O$ 0.6, $MgSO_4x7H_2O$ 1.2, $NaHCO_3$ 12, $KHCO_3$ 10, HEPES 10, Taurine 30, BDM 10, glucose 5.5, phenol-red 0.032 for 4 min at 37°C and pH 7.4. Thereafter, perfusion solution was switched to the same solution containing 7.5 mg/ml liberase 1 (Roche diagnostics, Mannheim, Germany), trypsin 0.6% and 0.125 mM $CaCl_2$, and perfusion was continued for about 3 min until the heart became flaccid. Ventricular tissue was removed, cut into small pieces and dispersed until no solid cardiac tissue was left. Ca reintroduction was performed carefully via stepwise increasing Ca-concentration from 0.1 mM to 0.8 mM finally making cardiac myocytes ready for further measurements. Cell length were estimated on an inverted microscope (Nikon Eclipse TE2000-U) by measuring myocyte length in pixel followed by a conversion in metric units as assessed in an earlier performed pixel/µm calibration.

Shortening and Ca^{2+} Measurements

Shortening and Ca^{2+} measurements were performed as described previously.[12,13] In brief, myocytes were loaded with fluo-3 by incubation with 10 µmol/L of the acetoxymethyl ester (AM) form of the dye for 15 min at room temperature in darkness. After loading, the cells were washed and afterwards superfused with normal Tyrode´s (NT) solution containing (mmol/L): 140 NaCl, 4 KCl, 5 HEPES, 1 $MgCl_2$, 10 glucose, and 1 $CaCl_2$ (37°C, pH 7.4). The dye was excited at a wavelength of 480±15 nm using a 75 W xenon arc lamp (Ushio, Japan) on the stage of the Nikon Eclipse TE200-U inverted microscope. Emitted fluorescence was measured using a photomultiplier (at 535±20 nm). Myocytes were field-stimulated (voltage 25% above threshold) at 1 Hz and 37°C until steady-state was achieved. Cells were transilluminated by red light (>650 nm) and shortening was measured using a sarcomere length detection system (IonOptix Corp, Milton, USA). SR Ca^{2+} content was estimated by rapid application of 10 mmol/L caffeine to cause complete SR Ca^{2+} release. Fractional SR Ca^{2+} release was quantitatively assessed by dividing the Ca^{2+} transient amplitude (F/F_0) recorded at 1 Hz just before application of caffeine by the caffeine-induced Ca^{2+} transient amplitude itself. In a subset of experiments for CaMKII inhibition were added to superfusion (µmol/L): 1 KN-93 (Seikagaku Corporation) and 1 KN-92 (Sigma) as an inactive control.

Confocal Ca^{2+} Measurements

Intact myocytes were loaded with 10 µmol/L fluo-4 AM for 15 min at room temperature. The cells were perfused with normal Tyrode´s solution containing 3 mmol/L $CaCl_2$ to de-esterify fluo-4 AM before starting the recordings. Ca^{2+} sparks were assessed by a laser scanning confocal microscope (LSM 5 Pascal, Zeiss, Germany) as previously reported.[12] Fluo-4 was excited by an argon ion laser (488 nm) and emitted fluorescence was collected through a 515 nm long-pass emission filter. Fluorescence images were recorded in line-scan mode with 512 pixels per line, pixel time 0.64 µs, pixel size 0.07 µm×0.07 µm, width of the scan 38.4 µm. Diastolic Ca^{2+} spark frequency (CaSpF) was measured following 0.5 Hz stimulation and normalized to cell volume and scan rate (pL-1*s-1). Peak of Ca^{2+} sparks were normalized as F/F_0.

Patch-Clamp measurements

Current-clamp measurements were performed at stepwise increased stimulation rates (0.5, 1, 2 and 4 Hz) to elicit action potentials (AP) on an inverted Nikon T 300 microscope using a HEKA EPC 10 patch-clamp-setup (Heka Electronics Inc, Lambrecht, Germany). Briefly, low-resistance pipettes (usually ~3 MΩ) were pulled and filled with an internal solution containing (in mM) K-aspartic acid 120, KCl 8, NaCl 7, $MgCl_2$ 1, Mg-ATP 5 and HEPES 10. Cells were superfused with an external solution containing (in mM) KCl 5.4, NaCl 135, $MgCl_2$ 1, HEPES 10 and Glucose 10 at physiological temperature (36±1°C) and Ca-concentration (1 mM). Cells were current-clamped to -75.8±0.8 mV (TG) or -74.4±0.8 mV in WT, respectively. When appropriate, CaMKII was blocked by adding 0.1 µM autopeptide 2-related inhibitory peptide (AiP, Sigma) to the pipette solution. In order to investigate the impact of L-type Ca^{2+} current on the action potential characteristics in TAC-cells in a subset of experiments the L-type Ca channel was blocked by Nifedipine (0.5 µM). In all experiments, myocytes were mounted on the stage of a microscope (Eclise TE2000-U, Nikon).

Patch-clamp experiments were performed using the EPC-10 amplifier and Patchmaster software (HEKA, Germany). Myocytes were measured in a recordings chamber mounted on the stage of a microscope (Nikon). I_{Ca} were recorded using the ruptured-patch whole-cell-patch clamp technique. After rupture, 5 min was allowed for equilibration of intracellular solution and cytosol before starting measurements. Fast and slow capacitance as well as series resistance were compensated for using the built in functions of Patchmaster.

For I_{Ca} recordings, the bath solution contained (mmol/L): 140 NaCl, 4 CsCl, 1 $MgCl_2$, 5 HEPES, 10 glucose and 1 $CaCl_2$ (23°C, pH 7.4, NaOH). Pipettes for I_{Ca} experiments were pulled to resistances of 2-2.5 MΩ when filled with intracellular solution containing (mmol/L): 105 CsCl, 20 HEPES, 5 BAPTA*4Cs, 2 di-bromo-BAPTA, 5 Mg-ATP, 1.49 $CaCl_2$ (23°C, pH 7.2, CsOH) and autopeptide 2-related inhibitory peptide (AiP, 0.1µM) for inhibition of CaMKII when appropriate. From a holding potential of -90mV, cells were briefly depolarized to -40 mV for 50 ms to inactivate Na^+-currents, then clamped to test potentials steps between -30 mV and +50 mV for a duration of 200 ms in 10 mV step increases with an interval of 1 s. Measured currents were normalized to membrane capacitance.

Human samples

Left ventricular samples (septal resections) were obtained from adult patients with severe, symptomatic aortic stenosis (n = 6, age 72 ± 5 years, left ventricular ejection fraction 60 ± 2%) undergoing aortic valve replacement. Premedication mostly consisted of angiotensin-converting enzyme inhibitors (4 patients), ß-blockers (3 patients), calcium channel antagonists (2 patients) and one patient received amiodarone. Only those patients were used where systolic function was preserved (EF>50%) and marked septal hypertrophy was present in order to allow morrow resection and reasonable investigations limited to only hypertrophied myocardium. All procedures involving humans were performed in compliance with the local ethical committee.

Table with patient datas of aortic stenosis samples

						Medication					
Gender	**Age**	**EF** (%)	**Septum** [mm]	**PWT** [mm]	**AOA** [cm^2]	**ACE**	**AT1**	**Diu**	**BB**	**AA**	**CA**
F	80	50	17	15	0.50	+	-	-	+	-	-
F	76	60	13	13	0.49	-	-	+	-	Amiodaron	-
F	81	60	13	13	0.68	+	-	-	+	-	-
M	60	65	n.a.	n.a.	0.56	+	-	-	+	-	-
M	57	65	12	12	0.40	+	-	-	+	-	+
F	81	60	13	13	0.50	+	-	-	-	-	+

Table: EF: ejecting fraction, PWT: posterior wall thickness; AOA: aortic opening area; ACE: ACE inhibitors; AT1: AT1-inhibitors, DIU: diuretis; BB: ß-blocker; AA: antiarhythmics; CA: catecholamines

Western immunoblot analysis

Frozen muscle strips or pieces of the left ventricle were thawed on ice in 50 µL of homogenization buffer and homogenized. Protein concentrations of the suspensions were determined and 20 µg of samples subjected to SDS-PAGE. Western blotting was carried out according to standard protocols, using antibodies against SERCA (ABR, Rockford, USA), P-AKT (NEB, Ipswich, USA), AKT (NEB), P-GSK (NEB), P-p38 (NEB), p38 (NEB), P-ERK (NEB), ERK (NEB), P-JNK (NEB), JNK (NEB), GSK (BD-Transduction Laboratories, San Jose, USA), CaMKII (a gift from Don M. Bers)[14], P-CaMKII (ABR), P-HDAC5 (Genescript, Piscataway, USA), Calsequestrin (ABR), GAPDH (BioTrend, cologne, Germany). For quantification an enhanced chemoluminescence detection system (Amersham) was used according to the manufacturer's instructions.

Quantitative mRNA measurement in the mouse myocardium

DNA-free total RNA was extracted from myocardial samples by a standard protocol with the RNeasy kit and RNase-free DNAse Set (Qiagen, Hilden, Germany). First-strand cDNA synthesis was carried out with iScript cDNA synthesis kit (BioRad, München, Germany) according to manufacturer's instructions. Real-time polymerase chain reactions (PCRs) were performed on a Biorad iQ-Cycler in a volume of 20 µL in a 96-well plate. The reaction mixture consisted of 1µl cDNA with 19µl SYBR GRN SUPERMIX (BioRad, München, Germany). After initial denaturation for 60 s at 95 °C, the cycling program consisted of 40 cycles of 95°C for 15s, 60°C for 10s and 72°C for 15s. Emission at 530 nm was measured at the end of each cycle. Primer sequences used were:

GAPDH	sense:	GCAGTGGCAAAGTGGAGATT,
	antisense:	TCTCCATGGTGGTGAAGACA;
BNP	sense:	TCTCCAGAGCAATTCAAGAT,
	antisense:	AACAACTTCAGTGCGTTACA;
MCIP	sense	ACTGGAAGGTGGTGTCCTTGTC,
	antisense:	TCCAGCTTGGGCTTGACTGAG.
SERCA	sense:	AGATGGTCCTGGCAGATGAC,
	antisense:	GTCCAGGTCTGGAGGATTGA;
MHC6	sense:	CCGGGTGATCTTCCAGCTAA
	antisense:	GCTCAGCACATC AAAGGCACT
MHC7	sense:	TCCCAAGGAGAGACGACTGTG
	antisense:	CCTTAAGCAGGTCGGCTGAGT
NCX	sense:	GGACCAACAGCTGGAGAGAG
	antisense:	GAAGCCAGGTCTCCAAGTAA
RYR2	sense:	TCTTAGCCATCCTCCACACCA
	antisense:	CTTCCGATGGCTGCT CTGTTA
PLB	sense:	AAGGAAGCTGTTCGGGTTCAG
	antisense:	TATAAAAGGGCC ACAGCGTCA

cDNAs with known concentrations were used to generate quantification standard curves. Expression data were normalized to GAPDH.

miR-microarray

Total RNA from mouse myocardial tissue was isolated using TRIzol Reagent from invitrogen according to the manufacturer´s protocol. RNA quality was confirmed using the Agilent Bioanalyzer. The samples were subjected to microarray labeling and hybridization on version 11.0 miRCURY LNA™ microRNA Arrays at Exiqon, Denmark, covering all microRNAs annotated in miRBase 11.0 miRBase at The Wellcome Trust Sanger Institute. Each Sample was labeled with Hy3 and assayed against a Hy5 labelled common reference sample containing a set of all samples. After background correction and LOESS normalization, data is expressed as log2(Hy3/Hy5) and replicates (6 for each experimental group) accordingly as log median ratio differences between the sample groups (delta LMR). For a two-tailed Students T-test calculated between the four sample groups (TAC sham, TAC verum, Shunt sham, Shunt verum). Here the miRs showing a significant regulation between intervention and sham in addition with a significant regulation between both interventions are shown.

Gene array hybridization

The amplification and labeling of the RNA samples were carried out according to the manufacturer's instructions (Affymetrix, Santa Clara, CA). Between one to three µg from each sample were synthesized into double-stranded cDNA using SuperScript transcriptase (Life Technologies, Inc., Carlsbad, CA) and with an oligo(dT)$_{24}$ primer containing a T7 RNA polymerase promoter (TIBMOL Biol, Berlin, Germany). Labeled complementary RNA (cRNA) was prepared from double-stranded cDNA by in vitro transcription using the T7 RNA polymerase. After cleanup (Rneasy, Qiagen, Hilden, Germany), the biotin-labeled cRNA was fragmented by alkaline treatment [40 mmol/L Trisacetate (pH 8.2), 100 mmol//L potassium acetate, and 50 mmol//L magnesium acetate] at 94°C for 35 minutes. Ten µg of each cRNA sample was hybridized for 16 hours at 45°C to an Affymetrix mouse 430 2.0 GeneChip array. Chips were washed and stained with streptavidin-phycoerythrin using the

GeneChip fluidics station 450 according to protocols recommended by Affymetrix. Finally, probe arrays were scanned using the Affymetrix GeneChip System confocal scanner 3000. Raw data were analyzed with the Affymetrix GeneChip Operating Software (GCOS) version 1.4.

Analysis of microarray gene data

The computational and statistical analysis of the microarray data was carried out using the R version 2.9.1 software[15] and the Bioconductor packages[16]. Pre-processing of the data was performed using the RMA algorithm[17]. Differentially expressed genes were identified by fitting a linear model and applying an empirical Bayesian method using the *limma* package[18]. Gene lists were generated selecting for genes with a FDR-adjusted *P* value threshold of 0.05. Gene set enrichment analysis (GSEA)[19,20] was performed using the *Category* and *GSEABase* packages for the evaluation of differential gene expression at the level of predefined gene sets based on prior biological knowledge. A non-specific filter from the *genefilter* package was applied to remove the control probes, probe sets without EntrezGene identification and genes represented by more than one probe set were collapsed to the probe set with the largest variability. The Kyoto Encyclopaedia of Genes and Genomes (KEGG) pathway database[21] was used to compile the gene sets and those with a size smaller than 10 genes were filtered out. The permutation distribution was computed based on 1000 permutations and a *P* value threshold of 0.025 was selected corresponding to a two-tailed hypothesis test at the 0.05 level.

Calculation of mean total wall stress

Wall stress was calculated according the law of Laplace ($\sigma = P * r/2w$)[22] with P the systolic or diastolic pressure, w the wall thickness and r half of the LVEDD or LVESD at 4 time points during the cardiac cycle (mid-systolic, end-systolic, mid-diastolic, end-diastolic). Wall and chamber dimension were measured at end-diastole and end-systole. Wall stress was further calculated at mid-systole and mid-diastole. Mean wall stress was calculated by the formula: $WS_{mean} = WS_{sys}*t_{sys} + WS_{dia}*t_{dia}$ with WS_{sys} = mean [$WS_{(1)} + WS_{(2)} + WS_{(3)}$], WS_{dia} = mean [$WS_{(4)} + WS_{(1)}$], t_{sys} and t_{dia} the proportional duration of systole or diastole on the complete cardiac cycle. Time durations were calculated from the pressure/volume curves.

For analysis of gene array based expression raw microarray data were imported into R version 2.9.1[9] and analyzed further with the Bioconductor packages.[10] Pathway analysis was performed taking the gene set enrichment analysis approach[13,14] using the *Category* and *GSEABase* Bioconductor packages querying the Kyoto Encyclopedia of Genes and Genomes pathway database.[15]

Figure I

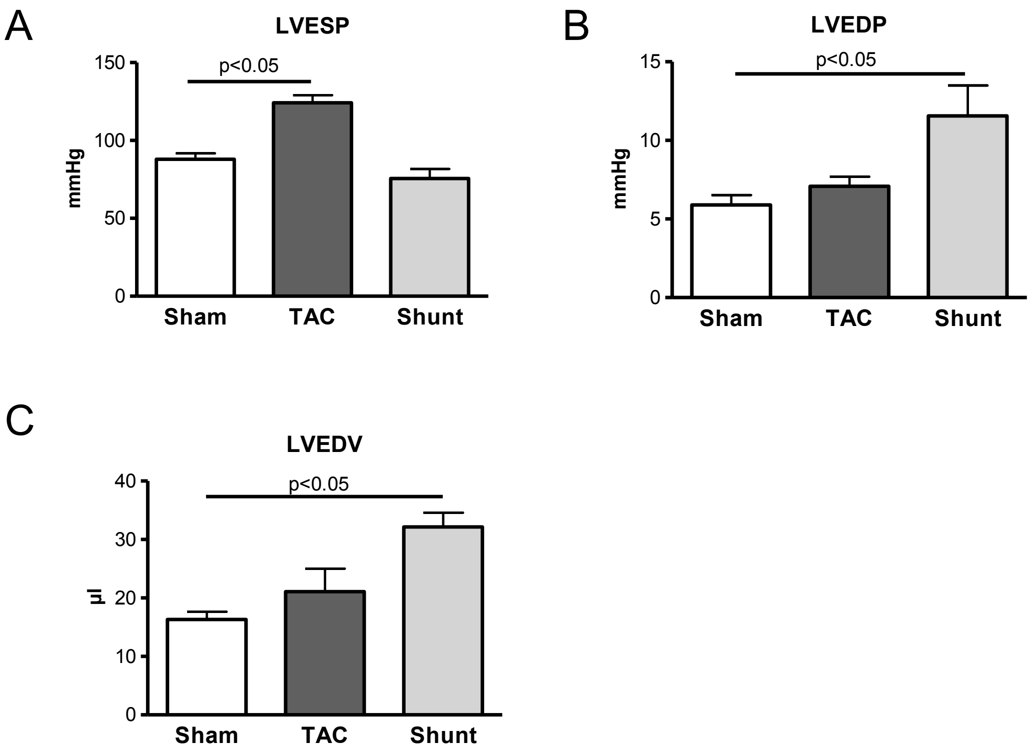
A
LVESP
150
100
50
0
mmHg
p<0.05
Sham
TAC
Shunt
B
LVEDP
15
10
5
0
mmHg
p<0.05
Sham
TAC
Shunt
C
LVEDV
40
30
20
10
0
μl
p<0.05
Sham
TAC
Shunt

Figure II

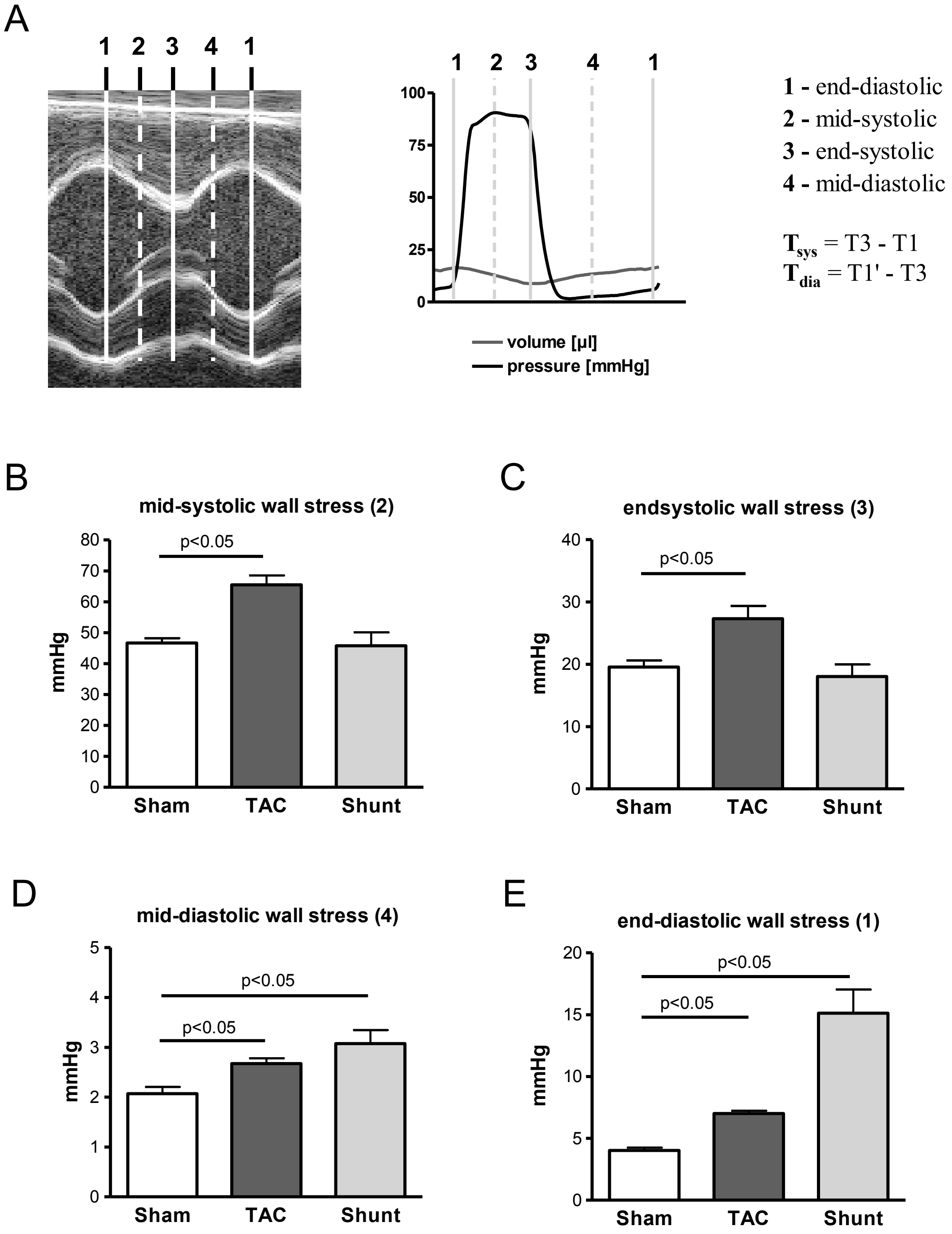
A
1 2 3 4 1
1 2 3 4 1
100
75
50
25
0
volume [µl]
pressure [mmHg]
1 - end-diastolic
2 - mid-systolic
3 - end-systolic
4 - mid-diastolic
T_{sys} = T3 - T1
T_{dia} = T1' - T3
B
mid-systolic wall stress (2)
mmHg
80
70
60
50
40
30
20
10
0
p<0.05
Sham
TAC
Shunt
C
endsystolic wall stress (3)
mmHg
40
30
20
10
0
p<0.05
Sham
TAC
Shunt
D
mid-diastolic wall stress (4)
mmHg
5
4
3
2
1
0
p<0.05
p<0.05
Sham
TAC
Shunt
E
end-diastolic wall stress (1)
mmHg
20
15
10
5
0
p<0.05
p<0.05
Sham
TAC
Shunt

Figure III

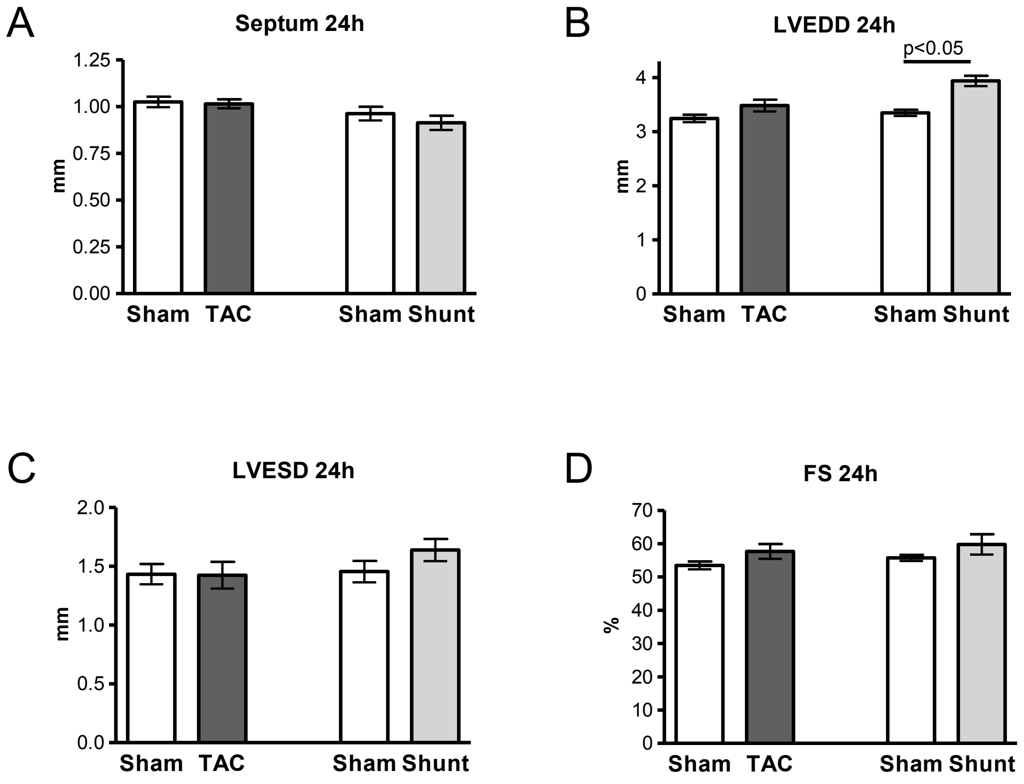
A
Septum 24h
mm
1.25
1.00
0.75
0.50
0.25
0.00
Sham TAC Sham Shunt
B
LVEDD 24h
p<0.05
mm
4
3
2
1
0
Sham TAC Sham Shunt
C
LVESD 24h
mm
2.0
1.5
1.0
0.5
0.0
Sham TAC Sham Shunt
D
FS 24h
%
70
60
50
40
30
20
10
0
Sham TAC Sham Shunt

Figure IV

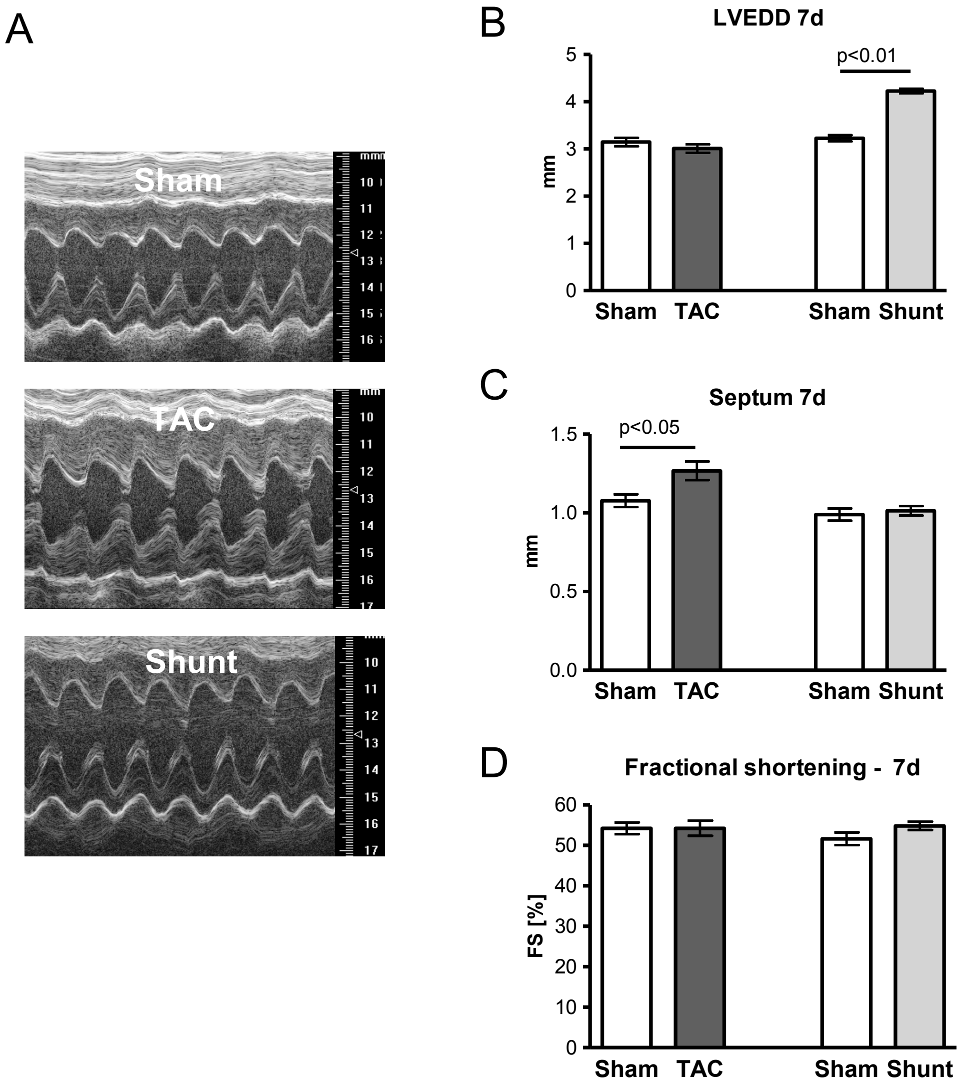
A
Sham
TAC
Shunt
B
LVEDD 7d
p<0.01
mm
0
1
2
3
4
5
Sham
TAC
Sham
Shunt
C
Septum 7d
p<0.05
mm
0.0
0.5
1.0
1.5
Sham
TAC
Sham
Shunt
D
Fractional shortening - 7d
FS [%]
0
10
20
30
40
50
60
Sham
TAC
Sham
Shunt

Figure V

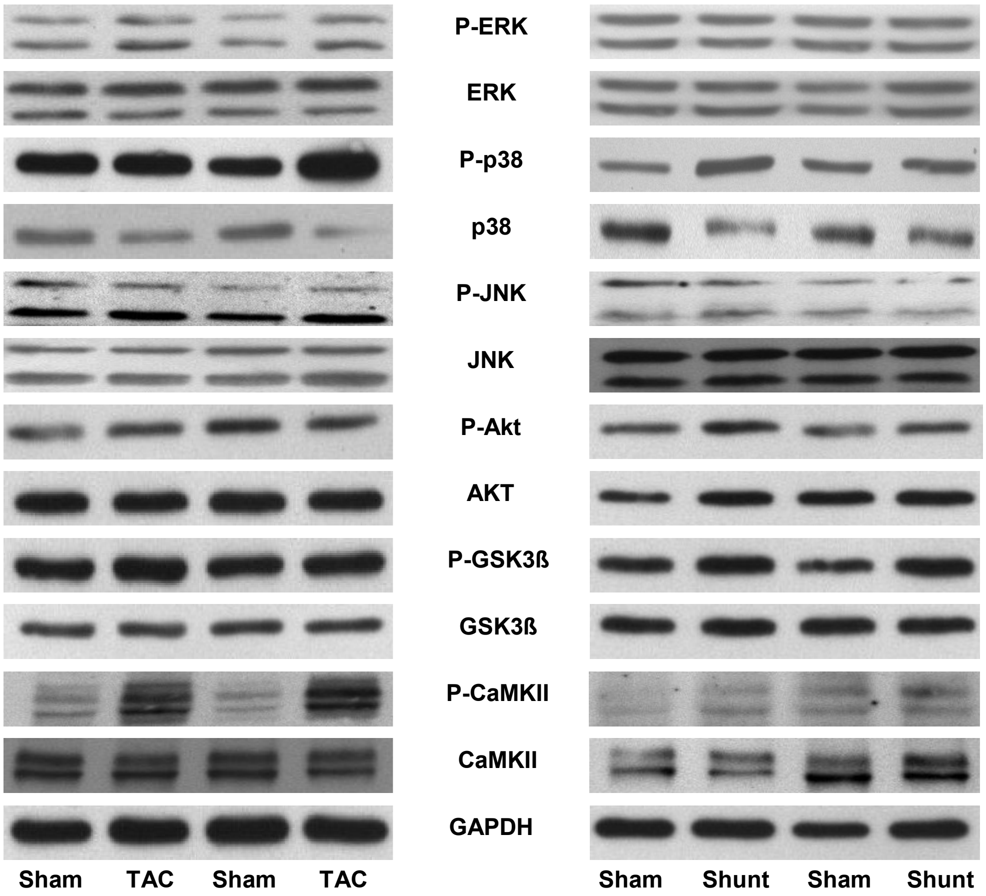
P-ERK
ERK
P-p38
p38
P-JNK
JNK
P-Akt
AKT
P-GSK3ß
GSK3ß
P-CaMKII
CaMKII
GAPDH
Sham
TAC
Sham
TAC
Sham
Shunt
Sham
Shunt

Figure VI

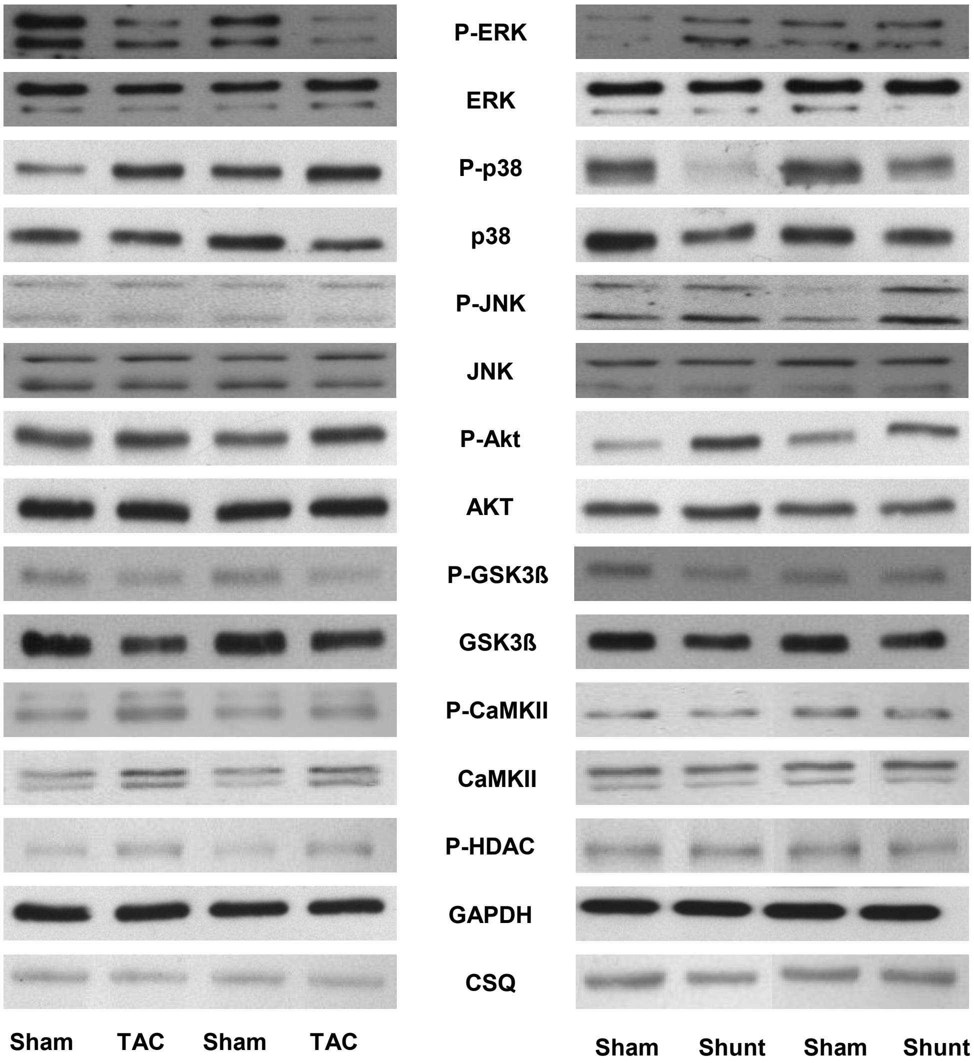
P-ERK
ERK
P-p38
p38
P-JNK
JNK
P-Akt
AKT
P-GSK3ß
GSK3ß
P-CaMKII
CaMKII
P-HDAC
GAPDH
CSQ
Sham
TAC
Sham
TAC
Sham
Shunt
Sham
Shunt

Figure VII

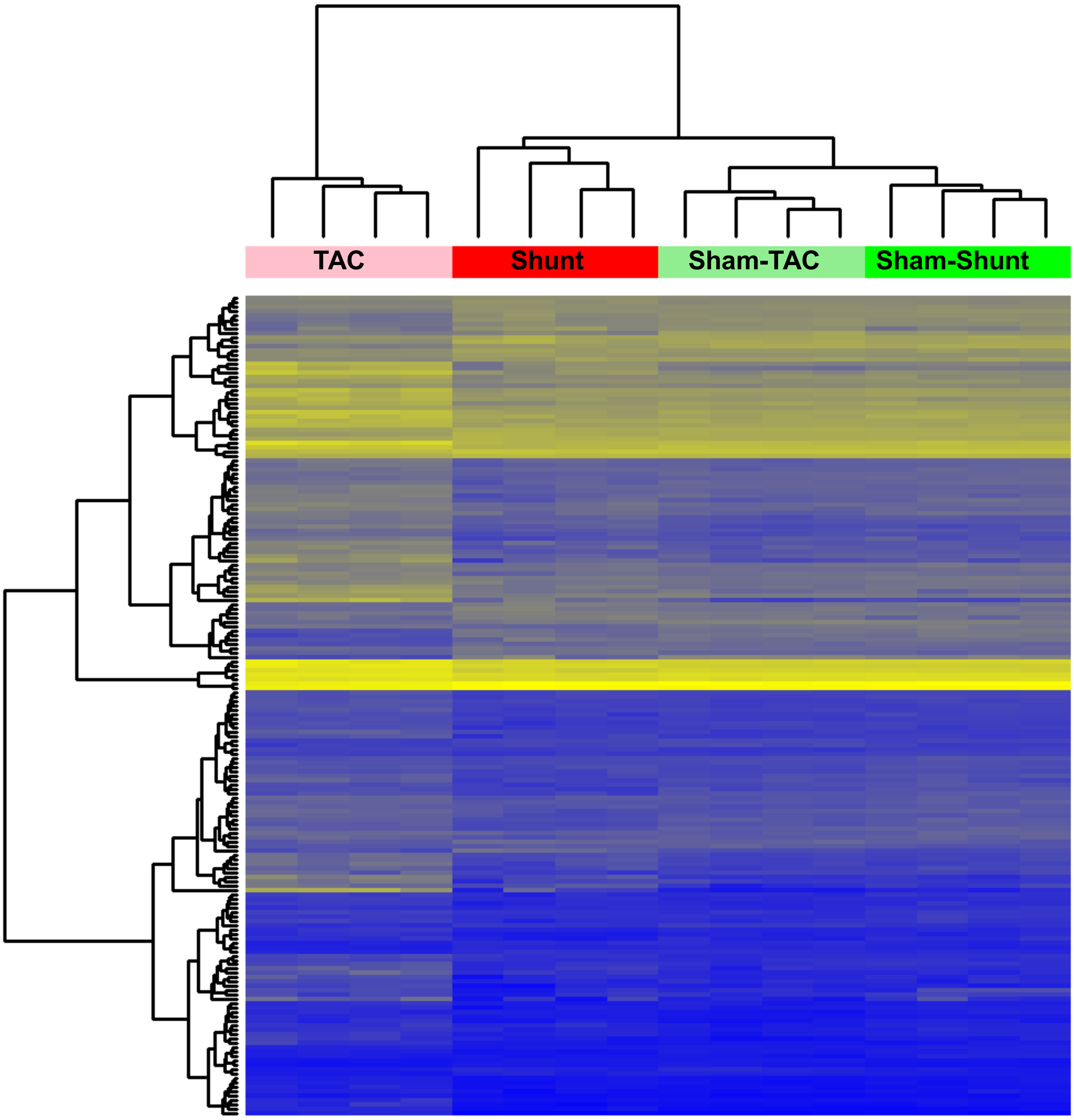

Figure Legend:

Suppl. Figure 1:

Parameters from in-vivo hemodynamic measurements in Sham, TAC and Shunt 6 hours after intervention (n=3 per group); **A**) left ventricular end-systolic pressure (LVESP); **B**) left ventricular end-diastolic pressure (LVEDP); **C**) left ventricular end-diastolic volume (LVEDV).

Suppl. Figure 2:

Wall stress calculation in Sham, TAC and Shunt 6 hours after intervention (n=3 per group); **A**) example of echocardiographic M-Mode, pressure and volume curves; **B**) mid-systolic wall stress; **C**) end-systolic wall stress; **D**) mid-diastolic wall stress;**E**) end-diastolic wall stress

Suppl. Figure 3:

Echocardiographic measurement in Sham, TAC and Shunt 24 hours after intervention (n=6 per group). **A**) Septum; **B**) left ventricular end-diastolic diameter (LVEDD); **C**) left ventricular end-systolic diameter (LVESD); **D**) Fractional shortening (FS)

Suppl. Figure 4:

Echocardiographic measurement in Sham, TAC and Shunt 7 days after intervention (n=8/10/7/7). **A**) Echocardiographic M-Mode registration of Sham, TAC and Shunt; **B**) left ventricular end-diastolic diameter (LVEDD; Shunt: +31%, p<0.01; TAC: no difference); **C**) Septum width (TAC +18% p<0.05, Shunt: no difference); **D**) Fractional shortening (FS).

Suppl. Figure 5:

Exemplary western blots of phosphorylated and total CaMK, MAPKs, Akt, GSK3ß and GAPDH expression 24 hours after intervention.

Suppl. Figure 6:

Exemplary western blots of phosphorylated and total CaMK, HDAC, MAPKs, Akt, GSK3ß, HDAC and GAPDH as well as calsequestrin expression 7 days after intervention

Suppl. Figure 7:

Analysis of gene expression in TAC, Shunt and corresponding Sham by microarrays (n=4 per group). Hierarchical clustering of the differentially regulated 187 probe sets and the individual animals in the appropriate groups (Heat map)

References:

1. Scheuermann-Freestone M, Freestone NS, Langenickel T, Höhnel K, Dietz R, Willenbrock R. A new model of congestive heart failure in the mouse due to chronic volume overload. Eur J Heart Fail. 2001;3:535-43.
2. Hu P, Zhang D, Swenson L, Chakrabarti G, Abel ED, Litwin SE. Minimally invasive aortic banding in mice: effects of altered cardiomyocyte insulin signaling during pressure overload. Am J Physiol Heart Circ Physiol 2003;285:H1261-9
3. Schmidt AG, Kadambi VJ, Ball N, Sato Y, Walsh RA, Kranias EG, Hoit BD. Cardiac-specific overexpression of calsequestrin results in left ventricular hypertrophy, depressed force-frequency relation and pulsus alternans in vivo. J Mol Cell Cardiol. 2000;32:1735-44.
4. El-Armouche A, Wittköpper K, Degenhardt F, Weinberger F, Didié M, Melnychenko I, Grimm M, Peeck M, Zimmermann WH, Unsöld B, Hasenfuss G, Dobrev D, Eschenhagen T. Phosphatase inhibitor-1-deficient mice are protected from catecholamine-induced arrhythmias and myocardial hypertrophy. Cardiovasc Res. 2008;80:396-406.
5. Bullock GR, Petrusz P. *Techniques in immunocytochemistry*. London; New York: Academic Press; 1982
6. Nakajima H, Nakajima HO, Tsai SC, Field LJ. Expression of mutant p193 and p53 permits cardiomyocyte cell cycle reentry after myocardial infarction in transgenic mice. *Circ Res.* 2004;94:1606-1614.
7. Nakajima H, Nakajima HO, Dembowsky K, Pasumarthi KB, Field LJ. Cardiomyocyte cell cycle activation ameliorates fibrosis in the atrium. *Circ Res.* 2006;98:141-148.

8. Pasumarthi KB, Nakajima H, Nakajima HO, Soonpaa MH, Field LJ. Targeted expression of cyclin D2 results in cardiomyocyte DNA synthesis and infarct regression in transgenic mice. *Circ Res.* 2005;96:110-118.

9. Soonpaa MH, Field LJ. Assessment of cardiomyocyte DNA synthesis in normal and injured adult mouse hearts. *Am J Physiol.* 1997;272:H220-226.

10. Dubowitz V, Sewry CA, Fitzsimons RB. *Muscle biopsy: a practical approach*. 2nd ed. London; Philadelphia: Baillière Tindall; 1985

11. Soonpaa MH, Koh GY, Klug MG, Field LJ. Formation of nascent intercalated disks between grafted fetal cardiomyocytes and host myocardium. *Science.* 1994;264:98-101.

12. Maier LS, Zhang T, Chen L, DeSantiago J, Brown JH, Bers DM. Transgenic CaMKIIdeltaC overexpression uniquely alters cardiac myocyte Ca2+ handling: reduced SR Ca2+ load and activated SR Ca2+ release. Circ Res. 2003;92:904-11.

13. Kohlhaas M, Zhang T, Seidler T, Zibrova D, Dybkova N, Steen A, Wagner S, Chen L, Brown JH, Bers DM, Maier LS. Increased sarcoplasmic reticulum calcium leak but unaltered contractility by acute CaMKII overexpression in isolated rabbit cardiac myocytes. Circ Res. 2006;98:235-44.

14. Huke S, Bers DM. Temporal dissociation of frequency-dependent acceleration of relaxation and protein phosphorylation by CaMKII. *J Mol Cell Cardiol.* 2007;42:590–599.

15. Ihaka R, Gentleman R. R: A language for data analysis and graphics. *J Comput Graph Stat* 1996;5:299-314.

16. Gentleman RC, Carey VJ, Bates DM, Bolstad B, Dettling M, Dudoit S*, et al.* Bioconductor: open software development for computational biology and bioinformatics. *Genome Biol* 2004;5:R80.

17. Irizarry RA, Hobbs B, Collin F, Beazer-Barclay YD, Antonellis KJ, Scherf U*, et al.* Exploration, normalization, and summaries of high density oligonucleotide array probe level data. *Biostatistics* 2003;4:249-264.

18. Smyth GK. Linear models and empirical bayes methods for assessing differential expression in microarray experiments. *Stat Appl Genet Mol Biol* 2004;3:Article3.

19. Mootha VK, Lindgren CM, Eriksson KF, Subramanian A, Sihag S, Lehar J*, et al.* PGC-1alpha-responsive genes involved in oxidative phosphorylation are coordinately downregulated in human diabetes. *Nat Genet* 2003;34:267-273.

20. Subramanian A, Tamayo P, Mootha VK, Mukherjee S, Ebert BL, Gillette MA*, et al.* Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. *Proc Natl Acad Sci U S A* 2005;102:15545-15550.

21. Kanehisa M, Goto S. KEGG: kyoto encyclopedia of genes and genomes. *Nucleic Acids Res* 2000;28:27-30.

22. Zierhut W, Studer R, Laurent D, Kästner S, Allegrini P, Whitebread S, Cumin F, Baum HP, de Gasparo M, Drexler H. Left ventricular wall stress and sarcoplasmic reticulum Ca(2+)-ATPase gene expression in renal hypertensive rats: dose-dependent effects of ACE inhibition and AT1-receptor blockade. *Cardiovasc Res*. 1996;31:758-68.

GENE ARRAY ANALYSIS

Table I

Upregulated in TAC vs. Sham

Affymetrix probe set identification	**Gene symbol**	**Gene name**	**Fold change**	**Adjusted *P* value**
1449254_at	Spp1	secreted phosphoprotein 1	53,75	0,0000
1460227_at	Timp1	tissue inhibitor of metalloproteinase 1	18,87	0,0000
1416342_at	Tnc	tenascin C	8,91	0,0000
1453898_at	Itgb1bp3	integrin beta 1 binding protein 3	7,30	0,0031
1455980_a_at	Gas2l3	growth arrest-specific 2 like 3	7,29	0,0002
1457296_at	Cilp	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	7,11	0,0003
1416121_at	Lox	lysyl oxidase	7,01	0,0000
1436329_at	Egr3	early growth response 3	6,91	0,0026
1419684_at	Ccl8	chemokine (C-C motif) ligand 8	6,51	0,0031
1426541_a_at	Endod1	endonuclease domain containing 1	6,42	0,0000
1423110_at	Col1a2	collagen, type I, alpha 2	6,32	0,0021
1424768_at	Cald1	caldesmon 1	6,29	0,0003
1455627_at	Col8a1	collagen, type VIII, alpha 1	5,99	0,0014
1423606_at	Postn	periostin, osteoblast specific factor	5,93	0,0210
1418440_at	Col8a1	collagen, type VIII, alpha 1	5,89	0,0005
1454694_a_at	Top2a	topoisomerase (DNA) II alpha	5,84	0,0367
1447819_x_at	Col8a1	collagen, type VIII, alpha 1	5,81	0,0001
1450625_at	Col5a2	collagen, type V, alpha 2	5,80	0,0111
1418949_at	Gdf15	growth differentiation factor 15	5,60	0,0048
1452242_at	Cep55	centrosomal protein 55	5,59	0,0332
1417457_at	Cks2	CDC28 protein kinase regulatory subunit 2	5,51	0,0343
1433543_at	Anln	anillin, actin binding protein	5,48	0,0197
1448228_at	Lox	lysyl oxidase	5,35	0,0013
1439740_s_at	Uck2	uridine-cytidine kinase 2	5,30	0,0000
1455494_at	Col1a1	collagen, type I, alpha 1	5,20	0,0020
1417458_s_at	Cks2	CDC28 protein kinase regulatory subunit 2	5,16	0,0358
1419100_at	Serpina3n	serine (or cysteine) peptidase inhibitor, clade A, member 3N	4,87	0,0185
1421694_a_at	Vcan	versican	4,84	0,0001
1418061_at	Ltbp2	latent transforming growth factor beta binding protein 2	4,83	0,0001
1427747_a_at	Lcn2	lipocalin 2	4,74	0,0445
1422437_at	Col5a2	collagen, type V, alpha 2	4,63	0,0011
1452968_at	Cthrc1	collagen triple helix repeat containing 1	4,61	0,0000
1421811_at	Thbs1	thrombospondin 1	4,58	0,0016
1439377_x_at	Cdc20	cell division cycle 20 homolog (S. cerevisiae)	4,53	0,0416
1450051_at	Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	4,38	0,0051
1448604_at	Uck2	uridine-cytidine kinase 2	4,37	0,0001

1428295_at	Synpo2l	synaptopodin 2-like	4,34	0,0173
1422789_at	Aldh1a2	aldehyde dehydrogenase family 1, subfamily A2	4,29	0,0059
1437744_at	Slitrk4	SLIT and NTRK-like family, member 4	4,28	0,0001
1450922_a_at	Tgfb2	transforming growth factor, beta 2	4,21	0,0000
1418441_at	Col8a1	collagen, type VIII, alpha 1	4,21	0,0016
1426642_at	Fn1	fibronectin 1	4,09	0,0102
1418728_at	Star	steroidogenic acute regulatory protein	4,07	0,0006
1423250_a_at	Tgfb2	transforming growth factor, beta 2	4,01	0,0000
1418476_at	Crlf1	cytokine receptor-like factor 1	4,00	0,0000
1449082_at	Mfap5	microfibrillar associated protein 5	3,98	0,0038
1416118_at	Trim59	tripartite motif-containing 59	3,95	0,0442
1452436_at	Loxl2	lysyl oxidase-like 2	3,94	0,0013
1437224_at	Rtn4	reticulon 4	3,90	0,0002
1455905_at	2610507B11 Rik	RIKEN cDNA 2610507B11 gene	3,88	0,0034
1439764_s_at	Igf2bp2	insulin-like growth factor 2 mRNA binding protein 2	3,88	0,0002
1423760_at	Cd44	CD44 antigen	3,87	0,0000
1450065_at	Adcy7	adenylate cyclase 7	3,87	0,0028
1423669_at	Col1a1	collagen, type I, alpha 1	3,85	0,0079
1437581_at	Zfp800	zinc finger protein 800	3,85	0,0009
1460208_at	Fbn1	fibrillin 1	3,81	0,0034
1440282_at	Tulp4	tubby like protein 4	3,77	0,0006
1452382_at	Dnm3os	dynamin 3, opposite strand	3,75	0,0030
1437244_at	Gas2l3	growth arrest-specific 2 like 3	3,73	0,0005
1436755_at	Itih5	inter-alpha (globulin) inhibitor H5	3,69	0,0006
1419598_at	Ms4a6d	membrane-spanning 4-domains, subfamily A, member 6D	3,67	0,0001
1460302_at	Thbs1	thrombospondin 1	3,65	0,0042
1445481_at	AI317158	expressed sequence AI317158	3,60	0,0140
1418188_a_at	Ramp2	receptor (calcitonin) activity modifying protein 2	3,53	0,0026
1421854_at	Fgl2	fibrinogen-like protein 2	3,53	0,0035
1419599_s_at	Ms4a6d	membrane-spanning 4-domains, subfamily A, member 6D	3,50	0,0002
1428942_at	Mt2	metallothionein 2	3,50	0,0062
1434411_at	Col12a1	collagen, type XII, alpha 1	3,49	0,0003
1416309_at	Nusap1	nucleolar and spindle associated protein 1	3,48	0,0381
1416600_a_at	Rcan1	regulator of calcineurin 1	3,47	0,0009
1444058_at	Dzip3	DAZ interacting protein 3, zinc finger	3,45	0,0005
1427682_a_at	Egr2	early growth response 2	3,45	0,0219
1427275_at	Smc4	structural maintenance of chromosomes 4	3,44	0,0012
1419276_at	Enpp1	ectonucleotide pyrophosphatase/phosphodiesterase 1	3,43	0,0001
1441946_at	Itih5	inter-alpha (globulin) inhibitor H5	3,41	0,0288
1426909_at	Uck2	uridine-cytidine kinase 2	3,38	0,0000
1418454_at	Mfap5	microfibrillar associated protein 5	3,34	0,0147
1422748_at	Zeb2	zinc finger E-box binding homeobox 2	3,31	0,0003
1422814_at	Aspm	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	3,30	0,0313
1420947_at	Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	3,29	0,0084
1431004_at	LOC100047339	similar to lysyl oxidase-like 2	3,28	0,0268
1421855_at	Fgl2	fibrinogen-like protein 2	3,27	0,0002
1450923_at	Tgfb2	transforming growth factor, beta 2	3,24	0,0000
1420973_at	Arid5b	AT rich interactive domain 5B (MRF1-like)	3,23	0,0055
1425951_a_at	Clec4n	C-type lectin domain family 4, member n	3,19	0,0010

1427683_at	Egr2	early growth response 2	3,17	0,0174
1425896_a_at	Fbn1	fibrillin 1	3,15	0,0101
1449388_at	Thbs4	thrombospondin 4	3,13	0,0111
1426808_at	Lgals3	lectin, galactose binding, soluble 3	3,12	0,0006
1419519_at	Igf1	insulin-like growth factor 1	3,10	0,0001
1438271_at	Lpp	LIM domain containing preferred translocation partner in lipoma	3,08	0,0045
1416221_at	Fstl1	follistatin-like 1	3,06	0,0142
1417695_a_at	Soat1	sterol O-acyltransferase 1	3,06	0,0032
1419627_s_at	Clec4n	C-type lectin domain family 4, member n	3,04	0,0004
1451922_at	Lman1l	lectin, mannose-binding 1 like	3,00	0,0006
1456062_at	Nppa	natriuretic peptide precursor type A	2,98	0,0135
1444031_at	Camk2d	calcium/calmodulin-dependent protein kinase II, delta	2,98	0,0002
1459984_at	Mia3	melanoma inhibitory activity 3	2,97	0,0111
1448259_at	Fstl1	follistatin-like 1	2,97	0,0208
1448352_at	Luzp1	leucine zipper protein 1	2,96	0,0009
1450377_at	Thbs1	thrombospondin 1	2,96	0,0203
1416318_at	Serpinb1a	serine (or cysteine) peptidase inhibitor, clade B, member 1a	2,95	0,0023
1417872_at	Fhl1	four and a half LIM domains 1	2,94	0,0001
1423162_s_at	Spred1	sprouty protein with EVH-1 domain 1, related sequence	2,93	0,0010
1439436_x_at	Incenp	inner centromere protein	2,90	0,0240
1449876_at	Prkg1	protein kinase, cGMP-dependent, type I	2,90	0,0101
1436343_at	Chd4	chromodomain helicase DNA binding protein 4	2,89	0,0003
1440339_at	Enpp1	ectonucleotide pyrophosphatase/phosphodiesterase 1	2,89	0,0043
1444671_at	Rasal2	RAS protein activator like 2	2,88	0,0036
1457666_s_at	Ifi202b	interferon activated gene 202B	2,88	0,0099
1459546_s_at	Enpp1	ectonucleotide pyrophosphatase/phosphodiesterase 1	2,86	0,0000
1419149_at	Serpine1	serine (or cysteine) peptidase inhibitor, clade E, member 1	2,86	0,0012
1451827_a_at	Nox4	NADPH oxidase 4	2,85	0,0072
1416666_at	Serpine2	serine (or cysteine) peptidase inhibitor, clade E, member 2	2,85	0,0001
1442340_x_at	Cyr61	cysteine rich protein 61	2,84	0,0234
1458439_a_at	Dzip3	DAZ interacting protein 3, zinc finger	2,84	0,0042
1424542_at	S100a4	S100 calcium binding protein A4	2,83	0,0002
1416529_at	Emp1	epithelial membrane protein 1	2,80	0,0027
1440801_s_at	Adrbk2	adrenergic receptor kinase, beta 2	2,80	0,0253
1427311_at	Bptf	bromodomain PHD finger transcription factor	2,80	0,0035
1453416_at	Gas2l3	growth arrest-specific 2 like 3	2,80	0,0054
1442082_at	C3ar1	complement component 3a receptor 1	2,78	0,0033
1437103_at	Igf2bp2	insulin-like growth factor 2 mRNA binding protein 2	2,77	0,0001
1435990_at	Adamts2	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 2	2,77	0,0005
1416661_at	Eif3a	eukaryotic translation initiation factor 3, subunit A	2,76	0,0099
1427256_at	Vcan	versican	2,76	0,0260
1447657_s_at	Synpo2l	synaptopodin 2-like	2,75	0,0451
1431098_at	Clip1	CAP-GLY domain containing linker protein 1	2,75	0,0113
1435585_at	Tceal7	transcription elongation factor A (SII)-like 7	2,74	0,0014
1454159_a_at	Igfbp2	insulin-like growth factor binding protein 2	2,74	0,0054
1434376_at	Cd44	CD44 antigen	2,74	0,0000
1449615_s_at	Hdlbp	high density lipoprotein (HDL) binding protein	2,72	0,0101
1426259_at	Pank3	pantothenate kinase 3	2,71	0,0002
1427735_a_at	Acta1	actin, alpha 1, skeletal muscle	2,71	0,0046

1456307_s_at	Adcy7	adenylate cyclase 7	2,70	0,0197
1438403_s_at	Malat1	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	2,70	0,0021
1437675_at	Slc8a1	solute carrier family 8 (sodium/calcium exchanger), member 1	2,70	0,0103
1460218_at	Cd52	CD52 antigen	2,70	0,0005
1426543_x_at	Endod1	endonuclease domain containing 1	2,68	0,0003
1448424_at	Frzb	frizzled-related protein	2,65	0,0059
1415988_at	Hdlbp	high density lipoprotein (HDL) binding protein	2,64	0,0131
1450355_a_at	Capg	capping protein (actin filament), gelsolin-like	2,64	0,0008
1442368_at	Kctd12b	potassium channel tetramerisation domain containing 12b	2,64	0,0325
1436659_at	Dclk1	doublecortin-like kinase 1	2,63	0,0105
1451939_a_at	Srpx	sushi-repeat-containing protein	2,63	0,0000
1436533_at	Trove2	TROVE domain family, member 2	2,62	0,0012
1418350_at	Hbegf	heparin-binding EGF-like growth factor	2,61	0,0049
1419621_at	Ankrd2	ankyrin repeat domain 2 (stretch responsive muscle)	2,61	0,0005
1443923_at	Akap13	A kinase (PRKA) anchor protein 13	2,60	0,0047
1448169_at	Krt18	keratin 18	2,58	0,0009
1458179_at	NA	NA	2,56	0,0002
1434479_at	Col5a1	collagen, type V, alpha 1	2,56	0,0119
1422124_a_at	Ptprc	protein tyrosine phosphatase, receptor type, C	2,55	0,0009
1436838_x_at	Cotl1	coactosin-like 1 (Dictyostelium)	2,54	0,0083
1424754_at	Ms4a7	membrane-spanning 4-domains, subfamily A, member 7	2,53	0,0449
1427276_at	Smc4	structural maintenance of chromosomes 4	2,53	0,0008
1415877_at	Dpysl3	dihydropyrimidinase-like 3	2,53	0,0056
1418189_s_at	Ramp2	receptor (calcitonin) activity modifying protein 2	2,53	0,0064
1418431_at	Kif5b	kinesin family member 5B	2,53	0,0212
1450035_a_at	Prpf40a	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	2,52	0,0415
1453593_at	Vgll3	vestigial like 3 (Drosophila)	2,52	0,0252
1423407_a_at	Fbln2	fibulin 2	2,51	0,0028
1444083_at	Ttn	titin	2,51	0,0002
1427582_at	Fgf6	fibroblast growth factor 6	2,50	0,0016
1425060_s_at	Clip1	CAP-GLY domain containing linker protein 1	2,49	0,0220
1417262_at	Ptgs2	prostaglandin-endoperoxide synthase 2	2,48	0,0004
1416805_at	1110032E23Rik	RIKEN cDNA 1110032E23 gene	2,48	0,0308
1459463_at	NA	NA	2,47	0,0054
1447658_x_at	Synpo2l	synaptopodin 2-like	2,46	0,0421
1450397_at	Mtap1b	microtubule-associated protein 1B	2,46	0,0014
1444620_at	NA	NA	2,46	0,0029
1449073_at	Flnc	filamin C, gamma	2,46	0,0000
1450241_a_at	Evi2a	ecotropic viral integration site 2a	2,46	0,0104
1436746_at	Wnk1	WNK lysine deficient protein kinase 1	2,46	0,0031
1452360_a_at	Jarid1a	jumonji, AT rich interactive domain 1A (Rbp2 like)	2,45	0,0064
1455271_at	OTTMUSG00000014994	predicted gene, OTTMUSG00000014994	2,44	0,0001
1443219_at	NA	NA	2,44	0,0135
1448553_at	Myh7	myosin, heavy polypeptide 7, cardiac muscle, beta	2,43	0,0440
1424727_at	Ccr5	chemokine (C-C motif) receptor 5	2,43	0,0016
1418666_at	Ptx3	pentraxin related gene	2,42	0,0258
1418237_s_at	Col18a1	collagen, type XVIII, alpha 1	2,42	0,0097
1417639_at	Slc22a4	solute carrier family 22 (organic cation transporter), member 4	2,41	0,0011
1457823_at	Cyr61	cysteine rich protein 61	2,40	0,0330

1416200_at	Il33	interleukin 33	2,40	0,0095
1455736_at	Mybpc2	myosin binding protein C, fast-type	2,40	0,0249
1443212_at	NA	NA	2,40	0,0070
1440516_at	NA	NA	2,40	0,0009
1447812_x_at	Flnc	filamin C, gamma	2,40	0,0000
1448383_at	Mmp14	matrix metallopeptidase 14 (membrane-inserted)	2,39	0,0004
1442832_at	Ankrd52	ankyrin repeat domain 52	2,39	0,0260
1424271_at	Dclk1	doublecortin-like kinase 1	2,39	0,0147
1443191_at	NA	NA	2,39	0,0033
1449154_at	Col11a1	collagen, type XI, alpha 1	2,38	0,0000
1455299_at	Vgll3	vestigial like 3 (Drosophila)	2,38	0,0071
1429660_s_at	Smc2	structural maintenance of chromosomes 2	2,38	0,0488
1457275_at	Synm	synemin, intermediate filament protein	2,38	0,0026
1418937_at	Dio2	deiodinase, iodothyronine, type II	2,38	0,0001
1434129_s_at	Lhfpl2	lipoma HMGIC fusion partner-like 2	2,38	0,0257
1446426_at	NA	NA	2,38	0,0417
1418018_at	Cpd	carboxypeptidase D	2,37	0,0088
1435477_s_at	Fcgr2b	Fc receptor, IgG, low affinity IIb	2,37	0,0264
1428936_at	Atp2b1	ATPase, Ca++ transporting, plasma membrane 1	2,37	0,0006
1437082_at	Akap9	A kinase (PRKA) anchor protein (yotiao) 9	2,37	0,0483
1425603_at	Tmem176a	transmembrane protein 176A	2,37	0,0000
1417496_at	Cp	ceruloplasmin	2,37	0,0354
1457980_x_at	Uck2	uridine-cytidine kinase 2	2,37	0,0000
1439012_a_at	Dck	deoxycytidine kinase	2,36	0,0306
1426755_at	Ckap4	cytoskeleton-associated protein 4	2,36	0,0122
1422864_at	Runx1	runt related transcription factor 1	2,36	0,0004
1460426_at	Pde4dip	phosphodiesterase 4D interacting protein (myomegalin)	2,36	0,0346
1424598_at	Ddx6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	2,35	0,0083
1416069_at	Pfkp	phosphofructokinase, platelet	2,35	0,0002
1448754_at	Rbp1	retinol binding protein 1, cellular	2,35	0,0070
1417379_at	Iqgap1	IQ motif containing GTPase activating protein 1	2,35	0,0001
1452417_x_at	LOC100047628	similar to Chain L, Structural Basis Of Antigen Mimicry In A Clinically Relevant Melanoma Antigen System	2,34	0,0460
1419431_at	Ereg	epiregulin	2,34	0,0057
1448591_at	Ctss	cathepsin S	2,34	0,0003
1450652_at	Ctsk	cathepsin K	2,33	0,0010
1419609_at	Ccr1	chemokine (C-C motif) receptor 1	2,33	0,0001
1451651_at	Vsig4	V-set and immunoglobulin domain containing 4	2,32	0,0269
1416658_at	Frzb	frizzled-related protein	2,32	0,0001
1427353_at	Clasp1	CLIP associating protein 1	2,32	0,0442
1417130_s_at	Angptl4	angiopoietin-like 4	2,31	0,0423
1456777_at	Mgam	maltase-glucoamylase	2,31	0,0000
1440315_at	Mbnl1	muscleblind-like 1 (Drosophila)	2,31	0,0194
1448803_at	Golga4	golgi autoantigen, golgin subfamily a, 4	2,30	0,0070
1416414_at	Emilin1	elastin microfibril interfacer 1	2,30	0,0148
1436983_at	Crebbp	CREB binding protein	2,29	0,0194
1426024_a_at	Dbn1	drebrin 1	2,29	0,0011
1437218_at	Fn1	fibronectin 1	2,29	0,0002
1456621_at	Fam13a	family with sequence similarity 13, member A	2,28	0,0039
1417623_at	Slc12a2	solute carrier family 12, member 2	2,28	0,0071
1427919_at	Srpx2	sushi-repeat-containing protein, X-linked 2	2,28	0,0126
1448406_at	Eid1	EP300 interacting inhibitor of differentiation 1	2,28	0,0021
1419665_a_at	Nupr1	nuclear protein 1	2,27	0,0044
1442977_at	NA	NA	2,27	0,0018

1428045_a_at	Elf2	E74-like factor 2	2,27	0,0040
1425832_a_at	Cxcr6	chemokine (C-X-C motif) receptor 6	2,26	0,0006
1454995_at	Ddah1	dimethylarginine dimethylaminohydrolase 1	2,26	0,0007
1427263_at	Xist	inactive X specific transcripts	2,26	0,0036
1457058_at	Adamts2	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 2	2,25	0,0003
1446894_at	NA	NA	2,25	0,0040
1457359_at	Inpp4b	inositol polyphosphate-4-phosphatase, type II	2,25	0,0443
1439956_at	NA	NA	2,24	0,0296
1421551_s_at	Ifi202b	interferon activated gene 202B	2,24	0,0054
1420372_at	Sntb2	syntrophin, basic 2	2,24	0,0023
1446127_at	Zeb1	zinc finger E-box binding homeobox 1	2,24	0,0005
1427699_a_at	Ptpn11	protein tyrosine phosphatase, non-receptor type 11	2,24	0,0106
1424927_at	Glipr1	GLI pathogenesis-related 1 (glioma)	2,23	0,0027
1437401_at	Igf1	insulin-like growth factor 1	2,23	0,0007
1437279_x_at	Sdc1	syndecan 1	2,23	0,0004
1455396_at	Atp8b1	ATPase, class I, type 8B, member 1	2,23	0,0009
1417828_at	Aqp8	aquaporin 8	2,23	0,0358
1458685_at	Garnl1	GTPase activating RANGAP domain-like 1	2,22	0,0416
1436240_at	NA	NA	2,22	0,0207
1439450_x_at	A230046K03Rik	RIKEN cDNA A230046K03 gene	2,22	0,0041
1451999_at	Ldb3	LIM domain binding 3	2,22	0,0101
1419249_at	Pftk1	PFTAIRE protein kinase 1	2,22	0,0029
1437104_at	Arfgef1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	2,22	0,0211
1427347_s_at	Tubb2a	tubulin, beta 2A	2,22	0,0163
1439274_at	A230083H22Rik	RIKEN cDNA A230083H22 gene	2,21	0,0358
1424325_at	Esco1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	2,21	0,0022
1418796_at	Clec11a	C-type lectin domain family 11, member a	2,21	0,0010
1418944_at	Cysltr1	cysteinyl leukotriene receptor 1	2,21	0,0031
1439970_at	NA	NA	2,21	0,0127
1420394_s_at	Lilrb4	leukocyte immunoglobulin-like receptor, subfamily B, member 4	2,21	0,0001
1418465_at	Ncf4	neutrophil cytosolic factor 4	2,21	0,0001
1443827_x_at	Fam20c	family with sequence similarity 20, member C	2,20	0,0007
1430695_at	Tlr4	toll-like receptor 4	2,20	0,0007
1425848_a_at	Dusp26	dual specificity phosphatase 26 (putative)	2,20	0,0063
1436312_at	Ikzf1	IKAROS family zinc finger 1	2,20	0,0103
1437222_x_at	Rrm2b	ribonucleotide reductase M2 B (TP53 inducible)	2,20	0,0038
1437009_a_at	Rnf115	ring finger protein 115	2,19	0,0001
1437158_at	Nipbl	Nipped-B homolog (Drosophila)	2,19	0,0016
1458802_at	Hivep3	human immunodeficiency virus type I enhancer binding protein 3	2,18	0,0013
1429810_at	4921505C17Rik	RIKEN cDNA 4921505C17 gene	2,18	0,0040
1459860_x_at	Trim2	tripartite motif-containing 2	2,18	0,0010
1437221_at	Rrm2b	ribonucleotide reductase M2 B (TP53 inducible)	2,18	0,0040
1434067_at	AI662270	expressed sequence AI662270	2,17	0,0074
1455886_at	Cbl	Casitas B-lineage lymphoma	2,16	0,0270
1439407_x_at	Tagln2	transgelin 2	2,16	0,0231
1417268_at	Cd14	CD14 antigen	2,16	0,0264
1457458_at	Zc3h4	zinc finger CCCH-type containing 4	2,16	0,0005
1419092_a_at	Slk	STE20-like kinase (yeast)	2,16	0,0115
1448558_a_at	Pla2g4a	phospholipase A2, group IVA (cytosolic, calcium-	2,16	0,0051

		dependent)		
1417721_s_at	Laptm5	lysosomal-associated protein transmembrane 5	2,15	0,0011
1455660_at	Csf2rb	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	2,15	0,0000
1438133_a_at	Cyr61	cysteine rich protein 61	2,15	0,0427
1418547_at	Tfpi2	tissue factor pathway inhibitor 2	2,15	0,0142
1442277_at	Chka	choline kinase alpha	2,15	0,0026
1430561_at	Dnajb14	DnaJ (Hsp40) homolog, subfamily B, member 14	2,14	0,0013
1423615_at	Rnf115	ring finger protein 115	2,14	0,0002
1442827_at	Tlr4	toll-like receptor 4	2,14	0,0002
1416687_at	Plod2	procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	2,13	0,0090
1451941_a_at	Fcgr2b	Fc receptor, IgG, low affinity IIb	2,13	0,0176
1428730_at	Krit1	KRIT1, ankyrin repeat containing	2,13	0,0014
1419666_x_at	Nupr1	nuclear protein 1	2,12	0,0034
1418349_at	Hbegf	heparin-binding EGF-like growth factor	2,12	0,0093
1455019_x_at	Ckap4	cytoskeleton-associated protein 4	2,12	0,0015
1436892_at	Spred2	sprouty-related, EVH1 domain containing 2	2,10	0,0046
1418674_at	Osmr	oncostatin M receptor	2,10	0,0002
1448617_at	Cd53	CD53 antigen	2,10	0,0001
1440461_at	NA	NA	2,10	0,0019
1454613_at	9430041P20Rik	RIKEN cDNA 9430041P20 gene	2,10	0,0497
1452649_at	Rtn4	reticulon 4	2,10	0,0000
1440804_at	Nktr	natural killer tumor recognition sequence	2,09	0,0192
1439928_at	NA	NA	2,09	0,0054
1441466_at	Sfrs10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	2,09	0,0081
1452392_a_at	Wipi1	WD repeat domain, phosphoinositide interacting 1	2,09	0,0098
1434413_at	Igf1	insulin-like growth factor 1	2,09	0,0024
1457731_at	Psip1	PC4 and SFRS1 interacting protein 1	2,09	0,0067
1421116_a_at	Rtn4	reticulon 4	2,09	0,0030
1443721_x_at	Sbno2	strawberry notch homolog 2 (Drosophila)	2,08	0,0030
1431293_a_at	Cldnd1	claudin domain containing 1	2,08	0,0007
1459457_at	Camk2d	calcium/calmodulin-dependent protein kinase II, delta	2,08	0,0001
1437419_at	Bmp2k	BMP2 inducible kinase	2,08	0,0007
1426471_at	Zfp52	zinc finger protein 52	2,08	0,0292
1423161_s_at	Spred1	sprouty protein with EVH-1 domain 1, related sequence	2,08	0,0000
1446688_at	NA	NA	2,08	0,0001
1421499_a_at	Ptpn14	protein tyrosine phosphatase, non-receptor type 14	2,07	0,0018
1423184_at	Itsn2	intersectin 2	2,07	0,0058
1452483_a_at	Cd44	CD44 antigen	2,07	0,0026
1444638_at	Ttn	titin	2,07	0,0170
1451064_a_at	Psat1	phosphoserine aminotransferase 1	2,07	0,0144
1451978_at	Loxl1	lysyl oxidase-like 1	2,07	0,0037
1430786_at	1110002E22Rik	RIKEN cDNA 1110002E22 gene	2,07	0,0003
1417688_at	Fam20c	family with sequence similarity 20, member C	2,06	0,0000
1448160_at	Lcp1	lymphocyte cytosolic protein 1	2,06	0,0257
1424504_at	Rab22a	RAB22A, member RAS oncogene family	2,05	0,0058
1422587_at	Tmem45a	transmembrane protein 45a	2,05	0,0300
1451569_at	Nr2c2	nuclear receptor subfamily 2, group C, member 2	2,05	0,0057
1456112_at	Tpr	translocated promoter region	2,05	0,0030
1437118_at	Usp7	ubiquitin specific peptidase 7	2,05	0,0217
1419754_at	Myo5a	myosin VA	2,05	0,0045
1416953_at	Ctgf	connective tissue growth factor	2,05	0,0293

1449175_at	Gpr65	G-protein coupled receptor 65	2,05	0,0031
1424217_at	Papola	poly (A) polymerase alpha	2,05	0,0045
1437811_x_at	NA	NA	2,04	0,0232
1430568_at	Zc3h13	zinc finger CCCH type containing 13	2,04	0,0164
1416498_at	Ppic	peptidylprolyl isomerase C	2,04	0,0488
1423352_at	Crispld1	cysteine-rich secretory protein LCCL domain containing 1	2,04	0,0052
1439168_at	Camk2d	calcium/calmodulin-dependent protein kinase II, delta	2,03	0,0002
1423160_at	Spred1	sprouty protein with EVH-1 domain 1, related sequence	2,03	0,0001
1427262_at	Xist	inactive X specific transcripts	2,03	0,0029
1423249_at	Nktr	natural killer tumor recognition sequence	2,03	0,0127
1424443_at	Tm6sf1	transmembrane 6 superfamily member 1	2,03	0,0318
1429954_at	Clec4a3	C-type lectin domain family 4, member a3	2,03	0,0195
1427298_at	Dnm3os	dynamin 3, opposite strand	2,03	0,0066
1455280_at	Frem1	Fras1 related extracellular matrix protein 1	2,03	0,0001
1448061_at	Msr1	macrophage scavenger receptor 1	2,03	0,0009
1450297_at	Il6	interleukin 6	2,02	0,0025
1418826_at	Ms4a6b	membrane-spanning 4-domains, subfamily A, member 6B	2,02	0,0373
1419220_at	Xirp1	xin actin-binding repeat containing 1	2,02	0,0023
1424770_at	Cald1	caldesmon 1	2,02	0,0014
1457493_at	Pten	phosphatase and tensin homolog	2,02	0,0017
1458912_at	NA	NA	2,02	0,0188
1448392_at	Sparc	secreted acidic cysteine rich glycoprotein	2,02	0,0438
1443602_at	NA	NA	2,02	0,0009
1434089_at	Synpo	synaptopodin	2,02	0,0122
1427910_at	Cst6	cystatin E/M	2,01	0,0141
1438992_x_at	Atf4	activating transcription factor 4	2,01	0,0404
1440729_at	Eps15	epidermal growth factor receptor pathway substrate 15	2,01	0,0003
1431162_a_at	Enah	enabled homolog (Drosophila)	2,00	0,0166
1438556_a_at	Tmod3	tropomodulin 3	2,00	0,0125
1418538_at	Kdelr3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	2,00	0,0015
1451161_a_at	Emr1	EGF-like module containing, mucin-like, hormone receptor-like sequence 1	2,00	0,0264
1456060_at	Maf	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog	1,99	0,0161
1439180_at	Ino80d	INO80 complex subunit D	1,99	0,0041
1422860_at	Nts	neurotensin	1,99	0,0477
1449168_a_at	Akap2	A kinase (PRKA) anchor protein 2	1,99	0,0129
1454890_at	Amot	angiomotin	1,99	0,0048
1421074_at	Cyp7b1	cytochrome P450, family 7, subfamily b, polypeptide 1	1,98	0,0040
1434239_at	Rrp12	ribosomal RNA processing 12 homolog (S. cerevisiae)	1,98	0,0016
1455269_a_at	Coro1a	coronin, actin binding protein 1A	1,98	0,0090
1419182_at	Svep1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	1,98	0,0003
1420855_at	Eln	elastin	1,97	0,0180
1449446_at	Ccdc59	coiled-coil domain containing 59	1,97	0,0076
1433944_at	1500017E21 Rik	RIKEN cDNA 1500017E21 gene	1,97	0,0011
1448620_at	Fcgr3	Fc receptor, IgG, low affinity III	1,97	0,0040
1424350_s_at	Lpgat1	lysophosphatidylglycerol acyltransferase 1	1,97	0,0037
1416695_at	Tspo	translocator protein	1,97	0,0001

1452722_a_at	Cul5	cullin 5	1,96	0,0007
1438476_a_at	Chd4	chromodomain helicase DNA binding protein 4	1,96	0,0015
1450915_at	Ap3b1	adaptor-related protein complex 3, beta 1 subunit	1,96	0,0105
1453855_at	Mxra7	matrix-remodelling associated 7	1,96	0,0034
1424674_at	Slc39a6	solute carrier family 39 (metal ion transporter), member 6	1,96	0,0013
1437719_x_at	A230046K03Rik	RIKEN cDNA A230046K03 gene	1,96	0,0178
1436778_at	Cybb	cytochrome b-245, beta polypeptide	1,96	0,0044
1447164_at	NA	NA	1,96	0,0234
1435343_at	Dock10	dedicator of cytokinesis 10	1,96	0,0104
1427966_at	Fam105b	family with sequence similarity 105, member B	1,95	0,0003
1421041_s_at	Gsta2	glutathione S-transferase, alpha 2 (Yc2)	1,95	0,0247
1438702_at	Flrt2	fibronectin leucine rich transmembrane protein 2	1,95	0,0054
1457639_at	Atp6v1h	ATPase, H+ transporting, lysosomal V1 subunit H	1,95	0,0006
1449632_s_at	Fkbp10	FK506 binding protein 10	1,95	0,0026
1449280_at	Esm1	endothelial cell-specific molecule 1	1,95	0,0404
1416065_a_at	Ankrd10	ankyrin repeat domain 10	1,95	0,0008
1460000_at	Shisa3	shisa homolog 3 (Xenopus laevis)	1,95	0,0107
1422528_a_at	Zfp36l1	zinc finger protein 36, C3H type-like 1	1,95	0,0057
1437284_at	Fzd1	frizzled homolog 1 (Drosophila)	1,94	0,0003
1437457_a_at	Mtpn	myotrophin	1,94	0,0040
1445824_at	Zfp458	zinc finger protein 458	1,94	0,0089
1456251_x_at	Tspo	translocator protein	1,94	0,0004
1428585_at	Actn1	actinin, alpha 1	1,94	0,0066
1452385_at	Usp53	ubiquitin specific peptidase 53	1,94	0,0048
1456489_at	Pcf11	cleavage and polyadenylation factor subunit homolog (S. cerevisiae)	1,94	0,0065
1420380_at	Ccl2	chemokine (C-C motif) ligand 2	1,94	0,0434
1421624_a_at	Enah	enabled homolog (Drosophila)	1,94	0,0046
1415806_at	Plat	plasminogen activator, tissue	1,94	0,0062
1416165_at	Rab31	RAB31, member RAS oncogene family	1,93	0,0004
1417876_at	Fcgr1	Fc receptor, IgG, high affinity I	1,93	0,0472
1442709_at	NA	NA	1,93	0,0044
1459804_at	Crebbp	CREB binding protein	1,93	0,0043
1419256_at	Spnb2	spectrin beta 2	1,93	0,0362
1452181_at	Ckap4	cytoskeleton-associated protein 4	1,93	0,0021
1438948_x_at	Tspo	translocator protein	1,93	0,0003
1452035_at	Col4a1	collagen, type IV, alpha 1	1,93	0,0079
1448550_at	Lbp	lipopolysaccharide binding protein	1,93	0,0102
1446550_at	Gspt1	G1 to S phase transition 1	1,92	0,0115
1448260_at	Uchl1	ubiquitin carboxy-terminal hydrolase L1	1,92	0,0442
1415859_at	Eif3c	eukaryotic translation initiation factor 3, subunit C	1,92	0,0243
1420970_at	Adcy7	adenylate cyclase 7	1,92	0,0104
1441262_at	NA	NA	1,92	0,0007
1448213_at	Anxa1	annexin A1	1,92	0,0122
1456014_s_at	Trpt1	tRNA phosphotransferase 1	1,92	0,0033
1427526_at	Fgfr1op2	FGFR1 oncogene partner 2	1,92	0,0125
1422903_at	Ly86	lymphocyte antigen 86	1,92	0,0424
1437339_s_at	Pcsk5	proprotein convertase subtilisin/kexin type 5	1,92	0,0021
1450792_at	Tyrobp	TYRO protein tyrosine kinase binding protein	1,91	0,0094
1418430_at	Kif5b	kinesin family member 5B	1,91	0,0034
1449227_at	Ch25h	cholesterol 25-hydroxylase	1,91	0,0152
1453860_s_at	Nr3c1	nuclear receptor subfamily 3, group C, member 1	1,91	0,0003
1436870_s_at	Afap1l2	actin filament associated protein 1-like 2	1,91	0,0324
1459929_at	Zfp568	zinc finger protein 568	1,91	0,0328

1418774_a_at	Atp7a	ATPase, Cu++ transporting, alpha polypeptide	1,91	0,0038
1423909_at	Tmem176a	transmembrane protein 176A	1,90	0,0066
1442061_at	Btbd7	BTB (POZ) domain containing 7	1,90	0,0069
1449201_at	Star	steroidogenic acute regulatory protein	1,90	0,0018
1421851_at	Mtap1b	microtubule-associated protein 1B	1,90	0,0246
1433242_at	5830415B17Rik	RIKEN cDNA 5830415B17 gene	1,90	0,0028
1442197_at	AI480624	expressed sequence AI480624	1,90	0,0026
1416801_at	Trpm7	transient receptor potential cation channel, subfamily M, member 7	1,90	0,0158
1430596_s_at	Vgll3	vestigial like 3 (Drosophila)	1,90	0,0427
1415943_at	Sdc1	syndecan 1	1,90	0,0063
1446565_at	NA	NA	1,90	0,0381
1428671_at	2200002D01Rik	RIKEN cDNA 2200002D01 gene	1,90	0,0281
1417821_at	D17H6S56E-5	DNA segment, Chr 17, human D6S56E 5	1,90	0,0025
1443863_at	Fndc3a	fibronectin type III domain containing 3A	1,89	0,0011
AFFX-b-ActinMur/M12481_M_at	Actb	actin, beta	1,89	0,0041
1440882_at	Lrp8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	1,89	0,0055
1433842_at	Lrrfip1	leucine rich repeat (in FLII) interacting protein 1	1,89	0,0029
1426261_s_at	Ugt1a6a	UDP glucuronosyltransferase 1 family, polypeptide A6A	1,89	0,0027
1427456_at	Wdfy3	WD repeat and FYVE domain containing 3	1,89	0,0354
1418572_x_at	Tnfrsf12a	tumor necrosis factor receptor superfamily, member 12a	1,89	0,0056
1422868_s_at	Gda	guanine deaminase	1,88	0,0014
1456506_at	Prpf38b	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	1,88	0,0025
1459641_at	NA	NA	1,88	0,0494
1453787_at	Txndc13	thioredoxin domain containing 13	1,88	0,0357
1426937_at	6330406I15Rik	RIKEN cDNA 6330406I15 gene	1,88	0,0329
1418760_at	Rdh11	retinol dehydrogenase 11	1,88	0,0016
1436319_at	Sulf1	sulfatase 1	1,88	0,0478
1423585_at	Polr2b	polymerase (RNA) II (DNA directed) polypeptide B	1,88	0,0088
1417419_at	Ccnd1	cyclin D1	1,88	0,0465
1429464_at	Prkaa2	protein kinase, AMP-activated, alpha 2 catalytic subunit	1,87	0,0313
1450401_at	Tgs1	trimethylguanosine synthase homolog (S. cerevisiae)	1,87	0,0024
1442395_at	NA	NA	1,87	0,0119
1439650_at	Rtn4	reticulon 4	1,87	0,0156
1426754_x_at	Ckap4	cytoskeleton-associated protein 4	1,87	0,0048
1445081_at	A930041I02Rik	RIKEN cDNA A930041I02 gene	1,87	0,0003
1456791_at	Zfp800	zinc finger protein 800	1,87	0,0163
1449682_s_at	Tubb2a-ps2	tubulin, beta 2a, pseudogene 2	1,86	0,0277
1436898_at	Sfpq	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	1,86	0,0018
1448673_at	Pvrl3	poliovirus receptor-related 3	1,86	0,0058
1417507_at	Cyb561	cytochrome b-561	1,86	0,0001
1443682_at	NA	NA	1,86	0,0197
1429508_at	2310057M21Rik	RIKEN cDNA 2310057M21 gene	1,86	0,0008
1416741_at	Col5a1	collagen, type V, alpha 1	1,85	0,0041

1418829_a_at	Eno2	enolase 2, gamma neuronal	1,85	0,0019
1419123_a_at	Pdgfc	platelet-derived growth factor, C polypeptide	1,85	0,0034
1456951_at	NA	NA	1,85	0,0077
1440106_at	NA	NA	1,85	0,0133
1430680_a_at	5830417I10 Rik	RIKEN cDNA 5830417I10 gene	1,85	0,0016
1441811_x_at	Tmem176a	transmembrane protein 176A	1,85	0,0038
1418024_at	Narg1	NMDA receptor-regulated gene 1	1,85	0,0292
1442038_at	Rbm26	RNA binding motif protein 26	1,85	0,0041
AFFX-b-ActinMur/M12481_5_at	Actb	actin, beta	1,85	0,0024
1448239_at	Hmox1	heme oxygenase (decycling) 1	1,85	0,0158
1417178_at	Gipc2	GIPC PDZ domain containing family, member 2	1,84	0,0001
1440999_at	Zfp697	zinc finger protein 697	1,84	0,0018
1424687_at	Heatr6	HEAT repeat containing 6	1,84	0,0050
1439672_at	NA	NA	1,84	0,0343
1448606_at	Lpar1	lysophosphatidic acid receptor 1	1,84	0,0035
1459635_at	NA	NA	1,84	0,0055
1418571_at	Tnfrsf12a	tumor necrosis factor receptor superfamily, member 12a	1,84	0,0084
1455096_at	Flrt2	fibronectin leucine rich transmembrane protein 2	1,84	0,0417
1458282_at	NA	NA	1,83	0,0256
1422910_s_at	Smc6	structural maintenance of chromosomes 6	1,83	0,0449
1417836_at	Gpx7	glutathione peroxidase 7	1,83	0,0045
1453269_at	Unc5b	unc-5 homolog B (C. elegans)	1,83	0,0009
1434891_at	Ptgfrn	prostaglandin F2 receptor negative regulator	1,83	0,0186
1438892_at	Dep1	diabetic embryopathy 1	1,83	0,0395
1449311_at	Bach1	BTB and CNC homology 1	1,83	0,0293
1437305_at	Zfp770	zinc finger protein 770	1,83	0,0107
1456102_a_at	Cul5	cullin 5	1,83	0,0018
1458308_at	Sbno2	strawberry notch homolog 2 (Drosophila)	1,83	0,0451
1457908_at	NA	NA	1,83	0,0092
1447870_x_at	1110002E22 Rik	RIKEN cDNA 1110002E22 gene	1,83	0,0003
1423547_at	Lyz2	lysozyme 2	1,83	0,0401
1444004_at	Thoc2	THO complex 2	1,83	0,0243
1441643_at	Mrz 03	membrane-associated ring finger (C3HC4) 3	1,83	0,0211
1416572_at	Mmp14	matrix metallopeptidase 14 (membrane-inserted)	1,82	0,0424
1452014_a_at	Igf1	insulin-like growth factor 1	1,82	0,0039
1438200_at	Sulf1	sulfatase 1	1,82	0,0291
1426777_a_at	Wasl	Wiskott-Aldrich syndrome-like (human)	1,82	0,0031
1439191_at	NA	NA	1,82	0,0078
1418296_at	Fxyd5	FXYD domain-containing ion transport regulator 5	1,82	0,0001
1416246_a_at	Coro1a	coronin, actin binding protein 1A	1,82	0,0147
1427076_at	Mpeg1	macrophage expressed gene 1	1,82	0,0001
1441677_at	NA	NA	1,82	0,0241
1436051_at	Myo5a	myosin VA	1,82	0,0094
1429658_a_at	Smc2	structural maintenance of chromosomes 2	1,82	0,0413
1420170_at	Myh9	myosin, heavy polypeptide 9, non-muscle	1,82	0,0023
1416120_at	Rrm2	ribonucleotide reductase M2	1,82	0,0431
1452595_at	Adamts4	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 4	1,82	0,0023
1449282_at	Cysltr1	cysteinyl leukotriene receptor 1	1,81	0,0095
1455399_at	Cnksr1	connector enhancer of kinase suppressor of Ras 1	1,81	0,0028
1429882_at	6820431F20	RIKEN cDNA 6820431F20 gene	1,81	0,0069

	Rik			
1427257_at	Vcan	versican	1,81	0,0012
1424704_at	Runx2	runt related transcription factor 2	1,81	0,0264
1459488_at	NA	NA	1,81	0,0130
1418424_at	Tnfaip6	tumor necrosis factor alpha induced protein 6	1,81	0,0024
1437162_at	NA	NA	1,81	0,0066
1452117_a_at	Fyb	FYN binding protein	1,81	0,0006
1450986_at	Nop58	NOP58 ribonucleoprotein homolog (yeast)	1,81	0,0054
1434599_a_at	Tjp2	tight junction protein 2	1,81	0,0045
1438688_at	Srrm2	serine/arginine repetitive matrix 2	1,81	0,0048
1421172_at	Adam12	a disintegrin and metallopeptidase domain 12 (meltrin alpha)	1,80	0,0407
1450093_s_at	Zbtb7a	zinc finger and BTB domain containing 7a	1,80	0,0187
1420985_at	Ash1l	ash1 (absent, small, or homeotic)-like (Drosophila)	1,80	0,0137
1419144_at	Cd163	CD163 antigen	1,80	0,0034
1457760_at	A930004J17Rik	RIKEN cDNA A930004J17 gene	1,80	0,0186
1442569_at	NA	NA	1,80	0,0049
1423065_at	Dnmt3a	DNA methyltransferase 3A	1,80	0,0139
1451596_a_at	Sphk1	sphingosine kinase 1	1,80	0,0322
1457357_at	Tlk2	tousled-like kinase 2 (Arabidopsis)	1,80	0,0431
1453698_at	6030451C04Rik	RIKEN cDNA 6030451C04 gene	1,80	0,0151
1419038_a_at	Csnk2a1	casein kinase 2, alpha 1 polypeptide	1,80	0,0151
1421375_a_at	S100a6	S100 calcium binding protein A6 (calcyclin)	1,80	0,0005
1452740_at	Myh10	myosin, heavy polypeptide 10, non-muscle	1,79	0,0268
1428663_at	5133401H06Rik	RIKEN cDNA 5133401H06 gene	1,79	0,0015
1452244_at	6330406I15Rik	RIKEN cDNA 6330406I15 gene	1,79	0,0003
1422803_at	Fstl3	follistatin-like 3	1,79	0,0231
1457708_at	Mbd4	methyl-CpG binding domain protein 4	1,79	0,0063
1440563_at	NA	NA	1,79	0,0005
1433434_at	AW551984	expressed sequence AW551984	1,79	0,0000
1453240_a_at	Gcap14	granule cell antiserum positive 14	1,79	0,0004
1438131_at	Fbxw2	F-box and WD-40 domain protein 2	1,79	0,0250
1441644_at	NA	NA	1,79	0,0237
1447621_s_at	Tmem173	transmembrane protein 173	1,79	0,0117
1431609_a_at	Acp5	acid phosphatase 5, tartrate resistant	1,79	0,0009
1436178_at	Leprel1	leprecan-like 1	1,79	0,0027
1418536_at	H2-Q7	histocompatibility 2, Q region locus 7	1,78	0,0483
1455834_x_at	Tacc3	transforming, acidic coiled-coil containing protein 3	1,78	0,0097
1435144_at	NA	NA	1,78	0,0009
1419015_at	Wisp2	WNT1 inducible signaling pathway protein 2	1,78	0,0015
1436904_at	Med13	mediator complex subunit 13	1,78	0,0029
1418269_at	Loxl3	lysyl oxidase-like 3	1,78	0,0038
1417869_s_at	Ctsz	cathepsin Z	1,78	0,0144
1442604_at	Ercc6	excision repair cross-complementing rodent repair deficiency, complementation group 6	1,78	0,0007
1440293_at	C230081A13Rik	RIKEN cDNA C230081A13 gene	1,78	0,0079
1451335_at	Plac8	placenta-specific 8	1,78	0,0051
1451537_at	Chi3l1	chitinase 3-like 1	1,78	0,0005
1451642_at	Kif1b	kinesin family member 1B	1,78	0,0158
1434875_a_at	Hmgn3	high mobility group nucleosomal binding domain 3	1,78	0,0097
1424051_at	Col4a2	collagen, type IV, alpha 2	1,78	0,0031

1433972_at	Camta1	calmodulin binding transcription activator 1	1,78	0,0026
1426446_at	6430548M08Rik	RIKEN cDNA 6430548M08 gene	1,77	0,0008
1444494_at	Kbtbd10	kelch repeat and BTB (POZ) domain containing 10	1,77	0,0023
1455795_at	Dse	dermatan sulfate epimerase	1,77	0,0093
1424769_s_at	Cald1	caldesmon 1	1,77	0,0163
1429331_at	4632427E13Rik	RIKEN cDNA 4632427E13 gene	1,77	0,0091
1455332_x_at	Fcgr2b	Fc receptor, IgG, low affinity IIb	1,77	0,0150
1422556_at	Gna13	guanine nucleotide binding protein, alpha 13	1,77	0,0322
1441001_at	AI225934	expressed sequence AI225934	1,77	0,0264
1449315_at	Odz3	odd Oz/ten-m homolog 3 (Drosophila)	1,77	0,0031
1426604_at	Rnasel	ribonuclease L (2', 5'-oligoisoadenylate synthetase-dependent)	1,77	0,0038
1448301_s_at	Serpinb1a	serine (or cysteine) peptidase inhibitor, clade B, member 1a	1,77	0,0033
1434068_s_at	AI662270	expressed sequence AI662270	1,77	0,0029
1420249_s_at	Ccl6	chemokine (C-C motif) ligand 6	1,77	0,0042
1437047_at	Zfp664	zinc finger protein 664	1,77	0,0150
1454200_at	Zeb2	zinc finger E-box binding homeobox 2	1,77	0,0187
1421187_at	Ccr2	chemokine (C-C motif) receptor 2	1,77	0,0014
1423060_at	Pa2g4	proliferation-associated 2G4	1,77	0,0050
1428896_at	Pdgfrl	platelet-derived growth factor receptor-like	1,77	0,0465
1417045_at	Bid	BH3 interacting domain death agonist	1,77	0,0023
1446624_at	Fktn	fukutin	1,76	0,0324
1449870_a_at	Atp6v0a2	ATPase, H+ transporting, lysosomal V0 subunit A2	1,76	0,0016
1419603_at	Ifi204	interferon activated gene 204	1,76	0,0216
1436986_at	Sntb2	syntrophin, basic 2	1,76	0,0001
1425098_at	Zfp106	zinc finger protein 106	1,76	0,0046
1456110_at	Ankrd11	ankyrin repeat domain 11	1,76	0,0231
1432216_s_at	Mpp7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	1,76	0,0171
1437208_at	Sep 10	septin 10	1,76	0,0023
1424265_at	Npl	N-acetylneuraminate pyruvate lyase	1,75	0,0368
1439040_at	Cenpe	centromere protein E	1,75	0,0284
1436040_at	Snora44	small nucleolar RNA, H/ACA box 44	1,75	0,0324
1417936_at	Ccl9	chemokine (C-C motif) ligand 9	1,75	0,0242
1442027_at	Nbeal1	neurobeachin like 1	1,75	0,0034
1424270_at	Dclk1	doublecortin-like kinase 1	1,75	0,0080
1434236_at	Zdhhc20	zinc finger, DHHC domain containing 20	1,75	0,0048
1422706_at	Pmepa1	prostate transmembrane protein, androgen induced 1	1,75	0,0007
1451716_at	Mafb	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)	1,75	0,0013
1435163_at	9030612M13Rik	RIKEN cDNA 9030612M13 gene	1,75	0,0021
1437671_x_at	Prss23	protease, serine, 23	1,75	0,0016
1448749_at	Plek	pleckstrin	1,74	0,0177
1436937_at	Rbms3	RNA binding motif, single stranded interacting protein	1,74	0,0001
1451458_at	Tmem2	transmembrane protein 2	1,74	0,0370
1435394_s_at	Rhoc	ras homolog gene family, member C	1,74	0,0025
1438303_at	Tgfb2	transforming growth factor, beta 2	1,74	0,0004
1446268_at	Cyth3	cytohesin 3	1,74	0,0100
1438684_at	Nuak1	NUAK family, SNF1-like kinase, 1	1,74	0,0085
1444295_at	Neo1	neogenin	1,74	0,0364
1450871_a_at	Bcat1	branched chain aminotransferase 1, cytosolic	1,74	0,0005
1420474_at	Mtpn	myotrophin	1,73	0,0161

1450656_at	Gna13	guanine nucleotide binding protein, alpha 13	1,73	0,0094
1441112_at	LOC667118	similar to Zinc finger BED domain containing protein 4	1,73	0,0246
1428463_a_at	Ppp2r5e	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	1,73	0,0101
1445306_at	NA	NA	1,73	0,0018
1417868_a_at	Ctsz	cathepsin Z	1,73	0,0393
1436236_x_at	Cotl1	coactosin-like 1 (Dictyostelium)	1,73	0,0108
1424801_at	Enah	enabled homolog (Drosophila)	1,73	0,0034
1453572_a_at	Plp2	proteolipid protein 2	1,73	0,0003
1444574_at	NA	NA	1,73	0,0341
1460159_at	Mysm1	myb-like, SWIRM and MPN domains 1	1,73	0,0026
1433529_at	E430002G05Rik	RIKEN cDNA E430002G05 gene	1,73	0,0128
1422340_a_at	Actg2	actin, gamma 2, smooth muscle, enteric	1,73	0,0004
1434020_at	Pdap1	PDGFA associated protein 1	1,73	0,0080
1443603_at	NA	NA	1,73	0,0056
1455870_at	Akap2	A kinase (PRKA) anchor protein 2	1,73	0,0203
1417214_at	Rab27b	RAB27b, member RAS oncogene family	1,73	0,0005
1428921_at	2810021B07Rik	RIKEN cDNA 2810021B07 gene	1,72	0,0106
1435890_at	Atl3	atlastin GTPase 3	1,72	0,0051
1422514_at	Aebp1	AE binding protein 1	1,72	0,0041
1455682_at	Abl2	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)	1,72	0,0358
1424800_at	Enah	enabled homolog (Drosophila)	1,72	0,0014
1440260_at	Ccdc58	coiled-coil domain containing 58	1,72	0,0177
1437308_s_at	F2r	coagulation factor II (thrombin) receptor	1,72	0,0000
1451175_at	Spcs3	signal peptidase complex subunit 3 homolog (S. cerevisiae)	1,72	0,0012
1451411_at	Gprc5b	G protein-coupled receptor, family C, group 5, member B	1,72	0,0052
1458299_s_at	Nfkbie	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	1,72	0,0045
1459350_at	NA	NA	1,71	0,0025
1436512_at	Arl4c	ADP-ribosylation factor-like 4C	1,71	0,0215
1419482_at	C3ar1	complement component 3a receptor 1	1,71	0,0442
1435644_at	Sh3pxd2b	SH3 and PX domains 2B	1,71	0,0125
1426505_at	Evi2a	ecotropic viral integration site 2a	1,71	0,0133
1452445_at	Slc41a2	solute carrier family 41, member 2	1,71	0,0008
1419625_at	Hspa1l	heat shock protein 1-like	1,71	0,0096
1452368_at	Bcr	breakpoint cluster region	1,70	0,0071
1417359_at	Mfap2	microfibrillar-associated protein 2	1,70	0,0211
1416313_at	Mllt11	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11	1,70	0,0034
1435597_at	Atad5	ATPase family, AAA domain containing 5	1,70	0,0232
1423311_s_at	Tpbg	trophoblast glycoprotein	1,70	0,0008
1434286_at	Trps1	trichorhinophalangeal syndrome I (human)	1,70	0,0448
1451621_at	Pppde1	PPPDE peptidase domain containing 1	1,70	0,0127
1423310_at	Tpbg	trophoblast glycoprotein	1,70	0,0007
1418599_at	Col11a1	collagen, type XI, alpha 1	1,70	0,0015
1447930_at	Baz1a	bromodomain adjacent to zinc finger domain 1A	1,70	0,0395
1436247_at	4632419I22Rik	RIKEN cDNA 4632419I22 gene	1,70	0,0497
1440351_at	NA	NA	1,70	0,0004
1427260_a_at	Tpm3	tropomyosin 3, gamma	1,70	0,0185
1448728_a_at	Nfkbiz	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	1,70	0,0105

1416379_at	Panx1	pannexin 1	1,70	0,0015
1424680_at	Fam26e	family with sequence similarity 26, member E	1,70	0,0173
1451022_at	Lrp6	low density lipoprotein receptor-related protein 6	1,69	0,0196
1426366_at	Eif2c2	eukaryotic translation initiation factor 2C, 2	1,69	0,0041
1425639_at	Adap2	ArfGAP with dual PH domains 2	1,69	0,0286
1422046_at	Itgam	integrin alpha M	1,69	0,0114
1416226_at	Arpc1b	actin related protein 2/3 complex, subunit 1B	1,69	0,0493
1422013_at	Clec4a2	C-type lectin domain family 4, member a2	1,69	0,0158
1434700_at	G2e3	G2/M-phase specific E3 ubiquitin ligase	1,69	0,0263
1434903_s_at	Il1rl2	interleukin 1 receptor-like 2	1,69	0,0097
1444075_at	Filip1	filamin A interacting protein 1	1,69	0,0131
1460086_at	Rc3h2	ring finger and CCCH-type zinc finger domains 2	1,69	0,0384
1439998_at	Jmjd1c	jumonji domain containing 1C	1,69	0,0269
1419537_at	Tcfec	transcription factor EC	1,69	0,0017
1446095_at	Airn	antisense Igf2r RNA	1,69	0,0174
1433982_at	Usp28	ubiquitin specific peptidase 28	1,69	0,0003
1418724_at	Cfi	complement component factor i	1,68	0,0029
1424065_at	Edem1	ER degradation enhancer, mannosidase alpha-like 1	1,68	0,0005
1426713_s_at	Eprs	glutamyl-prolyl-tRNA synthetase	1,68	0,0044
1435888_at	Egfr	epidermal growth factor receptor	1,68	0,0425
1448471_a_at	Ctla2a	cytotoxic T lymphocyte-associated protein 2 alpha	1,68	0,0062
1426542_at	Endod1	endonuclease domain containing 1	1,68	0,0006
1449195_s_at	Cxcl16	chemokine (C-X-C motif) ligand 16	1,68	0,0107
1419309_at	Pdpn	podoplanin	1,68	0,0162
1423570_at	Abcg1	ATP-binding cassette, sub-family G (WHITE), member 1	1,68	0,0243
1452158_at	Eprs	glutamyl-prolyl-tRNA synthetase	1,68	0,0053
1425565_at	Rest	RE1-silencing transcription factor	1,68	0,0170
1433796_at	Endod1	endonuclease domain containing 1	1,68	0,0266
1440163_at	Ccnk	cyclin K	1,68	0,0015
1440392_at	Akap13	A kinase (PRKA) anchor protein 13	1,68	0,0033
1444435_at	Vps13b	vacuolar protein sorting 13B (yeast)	1,68	0,0264
1436714_at	Lpp	LIM domain containing preferred translocation partner in lipoma	1,68	0,0062
1439741_x_at	Uck2	uridine-cytidine kinase 2	1,67	0,0104
1434513_at	Atp13a3	ATPase type 13A3	1,67	0,0259
1443675_at	NA	NA	1,67	0,0025
1421064_at	Mpp5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	1,67	0,0138
1452783_at	Fndc3b	fibronectin type III domain containing 3B	1,67	0,0097
1437473_at	Maf	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog	1,67	0,0115
1424607_a_at	100039204	predicted gene, 100039204	1,67	0,0057
1423771_at	Prkcdbp	protein kinase C, delta binding protein	1,67	0,0483
1444537_at	AI429363	expressed sequence AI429363	1,67	0,0008
1424187_at	Ccdc80	coiled-coil domain containing 80	1,67	0,0478
1449978_at	Zfy2	zinc finger protein 2, Y linked	1,67	0,0123
1443801_at	NA	NA	1,67	0,0274
1433716_x_at	Gfra2	glial cell line derived neurotrophic factor family receptor alpha 2	1,67	0,0495
1460004_x_at	Stx6	syntaxin 6	1,67	0,0377
1458148_at	Nlrc3	NLR family, CARD domain containing 3	1,67	0,0296
1435964_a_at	Taok3	TAO kinase 3	1,67	0,0041
1456250_x_at	Tgfbi	transforming growth factor, beta induced	1,66	0,0414
1437235_x_at	Lpp	LIM domain containing preferred translocation partner in lipoma	1,66	0,0011

1445499_at	Zc3h13	zinc finger CCCH type containing 13	1,66	0,0168
1424609_a_at	100039204	predicted gene, 100039204	1,66	0,0048
1418427_at	Kif5b	kinesin family member 5B	1,66	0,0150
1442251_at	Vcpip1	valosin containing protein (p97)/p47 complex interacting protein 1	1,66	0,0034
1448744_at	Galns	galactosamine (N-acetyl)-6-sulfate sulfatase	1,66	0,0015
1437503_a_at	Shisa5	shisa homolog 5 (Xenopus laevis)	1,66	0,0024
1420558_at	Selp	selectin, platelet	1,66	0,0256
1428967_at	Igf1r	insulin-like growth factor I receptor	1,66	0,0184
1426938_at	Nova1	neuro-oncological ventral antigen 1	1,66	0,0132
1444952_a_at	Nucks1	nuclear casein kinase and cyclin-dependent kinase substrate 1	1,66	0,0041
1455377_at	Ttll7	tubulin tyrosine ligase-like family, member 7	1,66	0,0489
1449455_at	Hck	hemopoietic cell kinase	1,66	0,0005
1440878_at	Runx1	runt related transcription factor 1	1,66	0,0004
1421045_at	Mrc2	mannose receptor, C type 2	1,66	0,0456
1424556_at	Pycr1	pyrroline-5-carboxylate reductase 1	1,66	0,0069
1420411_a_at	Pi4k2b	phosphatidylinositol 4-kinase type 2 beta	1,66	0,0043
1423341_at	Cspg4	chondroitin sulfate proteoglycan 4	1,66	0,0036
1421814_at	Msn	moesin	1,66	0,0006
1423948_at	Bag2	BCL2-associated athanogene 2	1,65	0,0028
1434316_at	Chsy1	chondroitin sulfate synthase 1	1,65	0,0067
1450714_at	Azin1	antizyme inhibitor 1	1,65	0,0069
1454849_x_at	Clu	clusterin	1,65	0,0321
1428572_at	Basp1	brain abundant, membrane attached signal protein 1	1,65	0,0452
1441594_at	NA	NA	1,65	0,0031
1434447_at	Met	met proto-oncogene	1,65	0,0007
1422638_s_at	Rassf5	Ras association (RalGDS/AF-6) domain family member 5	1,65	0,0059
1416871_at	Adam8	a disintegrin and metallopeptidase domain 8	1,65	0,0256
1424942_a_at	Myc	myelocytomatosis oncogene	1,65	0,0497
1460695_a_at	2010111I01 Rik	RIKEN cDNA 2010111I01 gene	1,65	0,0222
1456772_at	Ncf1	neutrophil cytosolic factor 1	1,65	0,0032
1454551_at	9530034D02 Rik	RIKEN cDNA 9530034D02 gene	1,65	0,0101
1448748_at	Plek	pleckstrin	1,65	0,0066
1444789_at	NA	NA	1,65	0,0054
1457270_at	Gas7	growth arrest specific 7	1,65	0,0083
1460116_s_at	Spred1	sprouty protein with EVH-1 domain 1, related sequence	1,64	0,0358
1418842_at	Hcls1	hematopoietic cell specific Lyn substrate 1	1,64	0,0371
1437545_at	Rcor1	REST corepressor 1	1,64	0,0020
1440771_at	Zkscan1	zinc finger with KRAB and SCAN domains 1	1,64	0,0096
1424208_at	Ptger4	prostaglandin E receptor 4 (subtype EP4)	1,64	0,0152
1450984_at	Tjp2	tight junction protein 2	1,64	0,0002
1443160_at	Sbf2	SET binding factor 2	1,64	0,0414
1425687_at	Cflar	CASP8 and FADD-like apoptosis regulator	1,64	0,0005
1449380_at	Pacsin1	protein kinase C and casein kinase substrate in neurons 1	1,64	0,0020
1451533_at	BC022687	cDNA sequence BC022687	1,64	0,0264
1417870_x_at	Ctsz	cathepsin Z	1,64	0,0450
1438861_at	Bnc2	basonuclin 2	1,64	0,0389
1425148_a_at	Snx6	sorting nexin 6	1,64	0,0001
1437759_at	Pfkp	phosphofructokinase, platelet	1,64	0,0054
1437544_at	Fubp1	far upstream element (FUSE) binding protein 1	1,64	0,0074

1456262_at	Rbm5	RNA binding motif protein 5	1,64	0,0363
1458655_at	NA	NA	1,64	0,0028
1456069_at	Dtna	dystrobrevin alpha	1,64	0,0154
1429831_at	Pik3ap1	phosphoinositide-3-kinase adaptor protein 1	1,63	0,0192
1459791_at	Dnajc1	DnaJ (Hsp40) homolog, subfamily C, member 1	1,63	0,0031
1451227_a_at	Slc10a3	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	1,63	0,0025
1421228_at	Ccl7	chemokine (C-C motif) ligand 7	1,63	0,0141
1428167_a_at	Mpzl1	myelin protein zero-like 1	1,63	0,0077
1438401_at	Ubn1	ubinuclein 1	1,63	0,0015
1426152_a_at	Kitl	kit ligand	1,63	0,0130
1418355_at	Nucb2	nucleobindin 2	1,63	0,0001
1436731_at	Zfp385b	zinc finger protein 385B	1,63	0,0026
1424349_a_at	Lpgat1	lysophosphatidylglycerol acyltransferase 1	1,63	0,0137
1418755_at	Tbx15	T-box 15	1,63	0,0051
1450852_s_at	F2r	coagulation factor II (thrombin) receptor	1,63	0,0020
1423846_x_at	Tuba1b	tubulin, alpha 1B	1,63	0,0026
1438407_at	Dsel	dermatan sulfate epimerase-like	1,63	0,0066
1458315_at	Epc1	enhancer of polycomb homolog 1 (Drosophila)	1,63	0,0353
1449298_a_at	Pde1a	phosphodiesterase 1A, calmodulin-dependent	1,63	0,0198
1417282_at	Mmp23	matrix metallopeptidase 23	1,63	0,0478
1452788_at	Ppp2r5e	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	1,63	0,0425
1417961_a_at	Trim30	tripartite motif-containing 30	1,63	0,0420
1444194_at	NA	NA	1,63	0,0095
1439205_at	Nfatc2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	1,62	0,0012
1436722_a_at	Actb	actin, beta	1,62	0,0059
1443768_at	Rhoa	ras homolog gene family, member A	1,62	0,0064
1452016_at	Alox5ap	arachidonate 5-lipoxygenase activating protein	1,62	0,0036
1417143_at	Lpar1	lysophosphatidic acid receptor 1	1,62	0,0045
1455324_at	Plcxd2	phosphatidylinositol-specific phospholipase C, X domain containing 2	1,62	0,0043
1425567_a_at	Anxa5	annexin A5	1,62	0,0078
1418729_at	Star	steroidogenic acute regulatory protein	1,62	0,0002
1451667_at	Fam20b	family with sequence similarity 20, member B	1,62	0,0059
1429321_at	Rnf149	ring finger protein 149	1,62	0,0006
1422555_s_at	Gna13	guanine nucleotide binding protein, alpha 13	1,62	0,0019
1417266_at	Ccl6	chemokine (C-C motif) ligand 6	1,62	0,0150
1457402_at	NA	NA	1,62	0,0293
1441063_at	Eif2c3	eukaryotic translation initiation factor 2C, 3	1,62	0,0010
1419585_at	Rp2h	retinitis pigmentosa 2 homolog (human)	1,62	0,0082
1420946_at	Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	1,62	0,0128
1436025_at	Ccdc88a	coiled coil domain containing 88A	1,62	0,0274
1448561_at	Ncf2	neutrophil cytosolic factor 2	1,62	0,0021
1443956_at	Zfp397	zinc finger protein 397	1,62	0,0045
1455287_at	Cdk6	cyclin-dependent kinase 6	1,61	0,0231
1438798_at	4931406P16 Rik	RIKEN cDNA 4931406P16 gene	1,61	0,0464
1447803_x_at	Capg	capping protein (actin filament), gelsolin-like	1,61	0,0357
1440991_at	Plekhg1	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	1,61	0,0031
1419004_s_at	Bcl2a1a	B-cell leukemia/lymphoma 2 related protein A1a	1,61	0,0015
1417084_at	Eif4ebp2	eukaryotic translation initiation factor 4E binding protein 2	1,61	0,0043
1416431_at	Tubb6	tubulin, beta 6	1,61	0,0323

1437322_at	Rbm4	RNA binding motif protein 4	1,61	0,0135
1433971_at	Camta1	calmodulin binding transcription activator 1	1,61	0,0297
1450637_a_at	Aebp1	AE binding protein 1	1,61	0,0079
1441137_at	Bicc1	bicaudal C homolog 1 (Drosophila)	1,61	0,0010
1450678_at	Itgb2	integrin beta 2	1,61	0,0023
1452497_a_at	Nfatc3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	1,61	0,0113
1456145_at	Dleu2	deleted in lymphocytic leukemia, 2	1,60	0,0455
1418883_a_at	Pabpc1	poly(A) binding protein, cytoplasmic 1	1,60	0,0035
1435241_at	Heatr5a	HEAT repeat containing 5A	1,60	0,0340
1435929_at	9630033F20 Rik	RIKEN cDNA 9630033F20 gene	1,60	0,0181
1453172_at	Hspa13	heat shock protein 70 family, member 13	1,60	0,0087
1423790_at	Dap	death-associated protein	1,60	0,0385
1439615_at	Gan	giant axonal neuropathy	1,60	0,0102
1433857_at	Fat1	FAT tumor suppressor homolog 1 (Drosophila)	1,60	0,0024
1448894_at	Akr1b8	aldo-keto reductase family 1, member B8	1,60	0,0021
1459266_at	NA	NA	1,60	0,0100
1437176_at	Nlrc5	NLR family, CARD domain containing 5	1,60	0,0150
1422168_a_at	Bdnf	brain derived neurotrophic factor	1,60	0,0078
1455732_at	2610510E02 Rik	RIKEN cDNA 2610510E02 gene	1,60	0,0031
1457488_at	B230339M05Rik	RIKEN cDNA B230339M05 gene	1,60	0,0057
1449839_at	Casp3	caspase 3	1,60	0,0384
1439196_at	Hook3	hook homolog 3 (Drosophila)	1,59	0,0004
1426301_at	Alcam	activated leukocyte cell adhesion molecule	1,59	0,0308
1460220_a_at	Csf1	colony stimulating factor 1 (macrophage)	1,59	0,0355
1420842_at	Ptprf	protein tyrosine phosphatase, receptor type, F	1,59	0,0118
1460188_at	Ptpn6	protein tyrosine phosphatase, non-receptor type 6	1,59	0,0084
1421545_a_at	Syne1	synaptic nuclear envelope 1	1,59	0,0150
1455869_at	NA	NA	1,59	0,0188
1420731_a_at	Csrp2	cysteine and glycine-rich protein 2	1,59	0,0360
1424893_at	Ndel1	nuclear distribution gene E-like homolog 1 (A. nidulans)	1,59	0,0500
1433761_at	Pde4dip	phosphodiesterase 4D interacting protein (myomegalin)	1,59	0,0023
1433536_at	Lrp11	low density lipoprotein receptor-related protein 11	1,59	0,0177
1423805_at	Dab2	disabled homolog 2 (Drosophila)	1,59	0,0243
1447851_x_at	Atp10a	ATPase, class V, type 10A	1,59	0,0203
1448967_at	Nipsnap3a	nipsnap homolog 3A (C. elegans)	1,59	0,0197
1448931_at	F2rl1	coagulation factor II (thrombin) receptor-like 1	1,59	0,0038
1426260_a_at	Ugt1a6a	UDP glucuronosyltransferase 1 family, polypeptide A6A	1,59	0,0405
1437872_at	Napepld	N-acyl phosphatidylethanolamine phospholipase D	1,59	0,0440
1434674_at	Lyst	lysosomal trafficking regulator	1,59	0,0177
1445850_at	Ppp1r12b	protein phosphatase 1, regulatory (inhibitor) subunit 12B	1,59	0,0146
1437884_at	Arl5b	ADP-ribosylation factor-like 5B	1,59	0,0437
1456357_at	A930041I02 Rik	RIKEN cDNA A930041I02 gene	1,58	0,0013
1451734_a_at	Dbn1	drebrin 1	1,58	0,0454
1460567_at	Rfx7	regulatory factor X, 7	1,58	0,0083
1453586_at	Entpd1	ectonucleoside triphosphate diphosphohydrolase 1	1,58	0,0264
1450629_at	Lima1	LIM domain and actin binding 1	1,58	0,0220
1420843_at	Ptprf	protein tyrosine phosphatase, receptor type, F	1,58	0,0145
1420697_at	Slc15a3	solute carrier family 15, member 3	1,58	0,0173

1415826_at	Atp6v1h	ATPase, H+ transporting, lysosomal V1 subunit H	1,58	0,0013
1426540_at	Endod1	endonuclease domain containing 1	1,58	0,0040
1456586_x_at	Mvp	major vault protein	1,58	0,0039
1441389_at	NA	NA	1,58	0,0320
1449591_at	Casp4	caspase 4, apoptosis-related cysteine peptidase	1,58	0,0057
1424343_a_at	Eif1a	eukaryotic translation initiation factor 1A	1,58	0,0028
1422062_at	Msr1	macrophage scavenger receptor 1	1,58	0,0082
1417128_at	Plekho1	pleckstrin homology domain containing, family O member 1	1,58	0,0006
1427986_a_at	Col16a1	collagen, type XVI, alpha 1	1,58	0,0497
1444456_at	9030425P06Rik	RIKEN cDNA 9030425P06 gene	1,58	0,0238
1426350_at	Mgat2	mannoside acetylglucosaminyltransferase 2	1,58	0,0152
1446906_at	C81615	expressed sequence C81615	1,58	0,0118
1434418_at	Lass6	LAG1 homolog, ceramide synthase 6	1,57	0,0216
1431320_a_at	Myo5a	myosin VA	1,57	0,0030
1453427_at	Csnk2a1	casein kinase 2, alpha 1 polypeptide	1,57	0,0146
1447824_x_at	Hspa5	heat shock protein 5	1,57	0,0363
1418035_a_at	Prim2	DNA primase, p58 subunit	1,57	0,0272
1456983_at	NA	NA	1,57	0,0038
1447649_x_at	Dnajc1	DnaJ (Hsp40) homolog, subfamily C, member 1	1,57	0,0118
1459571_at	NA	NA	1,57	0,0018
1457398_at	NA	NA	1,57	0,0049
1456310_a_at	2610002J02Rik	RIKEN cDNA 2610002J02 gene	1,57	0,0151
1440708_at	Myh9	myosin, heavy polypeptide 9, non-muscle	1,57	0,0253
1423306_at	2010002N04Rik	RIKEN cDNA 2010002N04 gene	1,57	0,0083
1418340_at	Fcer1g	Fc receptor, IgE, high affinity I, gamma polypeptide	1,57	0,0151
1436530_at	OTTMUSG00000000971	predicted gene, OTTMUSG00000000971	1,57	0,0186
1439108_at	Mll5	myeloid/lymphoid or mixed-lineage leukemia 5	1,57	0,0130
1444507_at	Usp53	ubiquitin specific peptidase 53	1,57	0,0447
1450904_at	Tmem167	transmembrane protein 167	1,57	0,0073
1450234_at	Ms4a6c	membrane-spanning 4-domains, subfamily A, member 6C	1,57	0,0380
1452082_at	6430548M08Rik	RIKEN cDNA 6430548M08 gene	1,57	0,0017
1450924_at	Hdgfrp3	hepatoma-derived growth factor, related protein 3	1,56	0,0354
1449117_at	Jund	Jun proto-oncogene related gene d	1,56	0,0041
1454607_s_at	Psat1	phosphoserine aminotransferase 1	1,56	0,0480
1418824_at	Arf6	ADP-ribosylation factor 6	1,56	0,0349
1449270_at	Plxdc2	plexin domain containing 2	1,56	0,0437
1457022_at	NA	NA	1,56	0,0011
1428418_s_at	Fam164a	family with sequence similarity 164, member A	1,56	0,0041
1428497_at	Secisbp2	SECIS binding protein 2	1,56	0,0056
1449874_at	Ly96	lymphocyte antigen 96	1,56	0,0181
1423331_a_at	Pvrl3	poliovirus receptor-related 3	1,56	0,0411
1428197_at	Tspan9	tetraspanin 9	1,56	0,0267
1427357_at	Cda	cytidine deaminase	1,56	0,0233
1455049_at	Igsf3	immunoglobulin superfamily, member 3	1,56	0,0018
1435331_at	Pyhin1	pyrin and HIN domain family, member 1	1,56	0,0014
1435284_at	Rtn4	reticulon 4	1,56	0,0253
1421408_at	Igsf6	immunoglobulin superfamily, member 6	1,56	0,0159
1429120_at	Lnp	limb and neural patterns	1,56	0,0324
1424657_at	Taok1	TAO kinase 1	1,56	0,0230

1457455_at	Suhw4	suppressor of hairy wing homolog 4 (Drosophila)	1,56	0,0187
1429178_at	Odz3	odd Oz/ten-m homolog 3 (Drosophila)	1,56	0,0081
1423885_at	Lamc1	laminin, gamma 1	1,56	0,0241
1435748_at	Gda	guanine deaminase	1,55	0,0066
1445337_at	Dnajc13	DnaJ (Hsp40) homolog, subfamily C, member 13	1,55	0,0197
1439455_x_at	Capza1	capping protein (actin filament) muscle Z-line, alpha 1	1,55	0,0401
1429768_at	Dtna	dystrobrevin alpha	1,55	0,0045
1420259_at	Pkp2	plakophilin 2	1,55	0,0100
1441930_x_at	Vat1	vesicle amine transport protein 1 homolog (T californica)	1,55	0,0025
1442233_at	NA	NA	1,55	0,0211
1422831_at	Fbn2	fibrillin 2	1,55	0,0371
1419161_a_at	Nox4	NADPH oxidase 4	1,55	0,0070
1426025_s_at	Laptm5	lysosomal-associated protein transmembrane 5	1,55	0,0151
1450734_at	Sec16b	SEC16 homolog B (S. cerevisiae)	1,55	0,0253
1419132_at	Tlr2	toll-like receptor 2	1,55	0,0009
1429521_at	Alkbh8	alkB, alkylation repair homolog 8 (E. coli)	1,55	0,0208
1450047_at	Hs6st2	heparan sulfate 6-O-sulfotransferase 2	1,55	0,0026
1418809_at	Pira1	paired-Ig-like receptor A1	1,55	0,0158
1439109_at	Ccdc68	coiled-coil domain containing 68	1,55	0,0011
1457534_at	NA	NA	1,55	0,0340
1435749_at	Gda	guanine deaminase	1,55	0,0119
1455160_at	LOC100042464	hypothetical protein LOC100042464	1,54	0,0487
1422875_at	Cd84	CD84 antigen	1,54	0,0029
1453550_a_at	Far1	fatty acyl CoA reductase 1	1,54	0,0243
1435472_at	Kremen1	kringle containing transmembrane protein 1	1,54	0,0151
1431834_a_at	Emilin1	elastin microfibril interfacer 1	1,54	0,0281
1441756_at	NA	NA	1,54	0,0187
1441994_at	Pcdhb16	protocadherin beta 16	1,54	0,0101
1434186_at	Lpar4	lysophosphatidic acid receptor 4	1,54	0,0449
1430404_at	Akap13	A kinase (PRKA) anchor protein 13	1,54	0,0349
1451065_a_at	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	1,54	0,0314
1447602_x_at	Sulf2	sulfatase 2	1,54	0,0033
1421075_s_at	Cyp7b1	cytochrome P450, family 7, subfamily b, polypeptide 1	1,54	0,0045
1429093_at	Ddi2	DNA-damage inducible protein 2	1,54	0,0323
1421073_a_at	Ptger4	prostaglandin E receptor 4 (subtype EP4)	1,54	0,0192
1440884_s_at	A530047J11Rik	RIKEN cDNA A530047J11 gene	1,54	0,0197
1422620_s_at	Ppap2a	phosphatidic acid phosphatase type 2A	1,54	0,0105
1448545_at	Sdc2	syndecan 2	1,54	0,0291
1416303_at	Litaf	LPS-induced TN factor	1,54	0,0427
1444411_at	NA	NA	1,54	0,0274
1428228_at	Pgm3	phosphoglucomutase 3	1,54	0,0403
1448660_at	Arhgdig	Rho GDP dissociation inhibitor (GDI) gamma	1,54	0,0013
1447849_s_at	Maf	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog	1,54	0,0236
1437451_at	Ecscr	endothelial cell-specific chemotaxis regulator	1,54	0,0152
AFFX-b-ActinMur/M12481_3_at	Actb	actin, beta	1,53	0,0083
1431057_a_at	Prss23	protease, serine, 23	1,53	0,0039
1438807_at	Hnrnpr	heterogeneous nuclear ribonucleoprotein R	1,53	0,0158
1428069_at	Cdca7	cell division cycle associated 7	1,53	0,0171
1420819_at	Sla	src-like adaptor	1,53	0,0184

1436222_at	Gas5	growth arrest specific 5	1,53	0,0130
1460069_at	Smc6	structural maintenance of chromosomes 6	1,53	0,0048
1442109_at	NA	NA	1,53	0,0186
1435476_a_at	Fcgr2b	Fc receptor, IgG, low affinity IIb	1,53	0,0007
1431127_at	Zbtb43	zinc finger and BTB domain containing 43	1,53	0,0034
1452424_at	Lpar4	lysophosphatidic acid receptor 4	1,53	0,0257
1460419_a_at	Prkcb	protein kinase C, beta	1,53	0,0435
1450841_at	Stt3a	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)	1,53	0,0042
1441372_at	5930405F01 Rik	RIKEN cDNA 5930405F01 gene	1,53	0,0138
1435089_at	2010111I01 Rik	RIKEN cDNA 2010111I01 gene	1,53	0,0100
1437820_at	Foxs1	forkhead box S1	1,53	0,0243
1455998_at	LOC667118	similar to Zinc finger BED domain containing protein 4	1,53	0,0226
1426784_at	Trim47	tripartite motif-containing 47	1,53	0,0413
1448452_at	Irf8	interferon regulatory factor 8	1,53	0,0096
1426397_at	Tgfbr2	transforming growth factor, beta receptor II	1,53	0,0002
1455824_x_at	Stt3a	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)	1,52	0,0085
1424603_at	Sumf1	sulfatase modifying factor 1	1,52	0,0313
1423274_at	Serpine3	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 3	1,52	0,0470
1440553_at	Mecr	mitochondrial trans-2-enoyl-CoA reductase	1,52	0,0101
1415951_at	Fkbp10	FK506 binding protein 10	1,52	0,0043
1449414_at	Zfp53	zinc finger protein 53	1,52	0,0409
1423693_at	Ela1	elastase 1, pancreatic	1,52	0,0044
1452982_at	Igf1r	insulin-like growth factor I receptor	1,52	0,0454
1457294_at	Tmtc3	transmembrane and tetratricopeptide repeat containing 3	1,52	0,0055
1451680_at	Srxn1	sulfiredoxin 1 homolog (S. cerevisiae)	1,52	0,0440
1456686_at	NA	NA	1,52	0,0033
1441653_at	Srcap	Snf2-related CREBBP activator protein	1,52	0,0145
1447176_at	NA	NA	1,52	0,0394
1433759_at	Dpy19l1	dpy-19-like 1 (C. elegans)	1,52	0,0160
1446324_at	NA	NA	1,52	0,0051
1431420_s_at	Prelid1	PRELI domain containing 1	1,52	0,0281
1423326_at	Entpd1	ectonucleoside triphosphate diphosphohydrolase 1	1,52	0,0386
1438721_a_at	Irf3	interferon regulatory factor 3	1,52	0,0162
1434600_at	Tjp2	tight junction protein 2	1,52	0,0040
1416808_at	Nid1	nidogen 1	1,52	0,0283
1455314_at	Lpp	LIM domain containing preferred translocation partner in lipoma	1,52	0,0161
1428176_at	S1pr2	sphingosine-1-phosphate receptor 2	1,52	0,0158
1440776_at	Limch1	LIM and calponin homology domains 1	1,52	0,0046
1455350_at	Tmem62	transmembrane protein 62	1,52	0,0144
1427539_a_at	Zwint	ZW10 interactor	1,52	0,0204
1459237_at	NA	NA	1,52	0,0225
1449297_at	Casp12	caspase 12	1,52	0,0195
1427537_at	Eppk1	epiplakin 1	1,52	0,0291
1444431_at	Rcsd1	RCSD domain containing 1	1,51	0,0317
1437278_a_at	Uba2	ubiquitin-like modifier activating enzyme 2	1,51	0,0012
1440790_x_at	NA	NA	1,51	0,0152
1433617_s_at	B4galt5	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	1,51	0,0031
1442659_at	Pcdh9	protocadherin 9	1,51	0,0225
1441683_at	NA	NA	1,51	0,0173

1458496_at	NA	NA	1,51	0,0429
1430516_at	4930428B01Rik	RIKEN cDNA 4930428B01 gene	1,51	0,0132
1450985_a_at	Tjp2	tight junction protein 2	1,51	0,0010
1435588_at	Wdfy1	WD repeat and FYVE domain containing 1	1,51	0,0066
1455814_x_at	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	1,51	0,0082
1418245_a_at	Rbm9	RNA binding motif protein 9	1,51	0,0149
1417400_at	Rai14	retinoic acid induced 14	1,51	0,0249
1420979_at	Pak1	p21 (CDKN1A)-activated kinase 1	1,51	0,0035
1417136_s_at	Srpk2	serine/arginine-rich protein specific kinase 2	1,51	0,0111
1435777_at	Itpripl2	inositol 1,4,5-triphosphate receptor interacting protein-like 2	1,51	0,0378
1429327_at	Sdccag1	serologically defined colon cancer antigen 1	1,51	0,0093
1417248_at	Ralbp1	ralA binding protein 1	1,51	0,0281
1431405_a_at	Cspp1	centrosome and spindle pole associated protein 1	1,51	0,0394
1426304_x_at	B4galt7	xylosylprotein beta1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I)	1,51	0,0425
1424442_a_at	Pja2	praja 2, RING-H2 motif containing	1,51	0,0152
1454120_a_at	Pcgf6	polycomb group ring finger 6	1,51	0,0149
1416811_s_at	Ctla2a	cytotoxic T lymphocyte-associated protein 2 alpha	1,51	0,0054
1425241_a_at	Wsb1	WD repeat and SOCS box-containing 1	1,51	0,0306
1425556_at	Crkrs	CDC2-related kinase, arginine/serine-rich	1,51	0,0104
1438242_at	Usp40	ubiquitin specific peptidase 40	1,51	0,0469
1423829_at	Fam49b	family with sequence similarity 49, member B	1,50	0,0009
1435266_at	A930041I02Rik	RIKEN cDNA A930041I02 gene	1,50	0,0123
1460600_at	AA414768	expressed sequence AA414768	1,50	0,0034
1448123_s_at	Tgfbi	transforming growth factor, beta induced	1,50	0,0468
1424749_at	Wdfy1	WD repeat and FYVE domain containing 1	1,50	0,0497
1447903_x_at	Ap1s2	adaptor-related protein complex 1, sigma 2 subunit	1,50	0,0176
1454788_at	Arl4c	ADP-ribosylation factor-like 4C	1,50	0,0161
1421186_at	Ccr2	chemokine (C-C motif) receptor 2	1,50	0,0009
1460247_a_at	Skp2	S-phase kinase-associated protein 2 (p45)	1,50	0,0199
1443491_at	NA	NA	1,50	0,0202
1429433_at	Bat2d	BAT2 domain containing 1	1,50	0,0244
1459283_at	6430510B20Rik	RIKEN cDNA 6430510B20 gene	1,50	0,0424
1430152_at	Eps15	epidermal growth factor receptor pathway substrate 15	1,50	0,0028
1440290_at	ENSMUSG00000056771	predicted gene, ENSMUSG00000056771	1,50	0,0296
1425673_at	Lpp	LIM domain containing preferred translocation partner in lipoma	1,50	0,0057
1454899_at	Lpp	LIM domain containing preferred translocation partner in lipoma	1,50	0,0151
1417921_at	2610029G23Rik	RIKEN cDNA 2610029G23 gene	1,50	0,0023
1439440_x_at	Twf2	twinfilin, actin-binding protein, homolog 2 (Drosophila)	1,50	0,0183
1436336_at	Ptrh1	peptidyl-tRNA hydrolase 1 homolog (S. cerevisiae)	1,50	0,0017
1446798_at	Map4k3	mitogen-activated protein kinase kinase kinase kinase 3	1,50	0,0383
1444337_at	NA	NA	1,50	0,0162
1444279_at	Huwe1	HECT, UBA and WWE domain containing 1	1,50	0,0331
1422730_at	Limd1	LIM domains containing 1	1,50	0,0428
1417028_a_at	Trim2	tripartite motif-containing 2	1,50	0,0417
1446518_at	NA	NA	1,50	0,0264
1438151_x_at	Zdhhc14	zinc finger, DHHC domain containing 14	1,50	0,0041

1451715_at	Mafb	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)	1,50	0,0177
1448199_at	Ankrd10	ankyrin repeat domain 10	1,50	0,0007
1422637_at	Rassf5	Ras association (RalGDS/AF-6) domain family member 5	1,50	0,0072
1448129_at	Arpc5	actin related protein 2/3 complex, subunit 5	1,50	0,0040
1431339_a_at	Efhd2	EF hand domain containing 2	1,50	0,0283
1418718_at	Cxcl16	chemokine (C-X-C motif) ligand 16	1,49	0,0075
1434232_a_at	2610030H06 Rik	RIKEN cDNA 2610030H06 gene	1,49	0,0378
1438212_at	Usp37	ubiquitin specific peptidase 37	1,49	0,0086
1455992_at	Vgll4	vestigial like 4 (Drosophila)	1,49	0,0324
1425548_a_at	Lst1	leukocyte specific transcript 1	1,49	0,0086
1454158_at	Mpp7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	1,49	0,0328
1418562_at	Sf3b1	splicing factor 3b, subunit 1	1,49	0,0101
1457658_x_at	Anxa4	annexin A4	1,49	0,0289
1440975_at	Mxra7	matrix-remodelling associated 7	1,49	0,0075
1448618_at	Mvp	major vault protein	1,49	0,0086
1420988_at	Polh	polymerase (DNA directed), eta (RAD 30 related)	1,49	0,0204
1459766_x_at	Sf1	splicing factor 1	1,49	0,0291
1438426_at	Shisa4	shisa homolog 4 (Xenopus laevis)	1,49	0,0109
1418778_at	Ccdc109b	coiled-coil domain containing 109B	1,49	0,0198
1455915_at	Galnt4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4	1,49	0,0330
1420832_at	Qsox1	quiescin Q6 sulfhydryl oxidase 1	1,49	0,0002
1449360_at	Csf2rb2	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage)	1,49	0,0020
1418049_at	Ltbp3	latent transforming growth factor beta binding protein 3	1,49	0,0343
1439953_at	Pmm2	phosphomannomutase 2	1,49	0,0450
1433623_at	Zfp367	zinc finger protein 367	1,49	0,0150
1457484_at	D930050J11	hypothetical D930050J11	1,49	0,0110
1444481_at	NA	NA	1,49	0,0054
1426168_a_at	Tcra	T-cell receptor alpha chain	1,49	0,0159
1441081_a_at	1110038B12 Rik	RIKEN cDNA 1110038B12 gene	1,49	0,0346
1429019_s_at	Pon2	paraoxonase 2	1,49	0,0345
1421366_at	Clec5a	C-type lectin domain family 5, member a	1,49	0,0440
1449027_at	Rhou	ras homolog gene family, member U	1,49	0,0111
1460084_at	NA	NA	1,49	0,0071
1437000_at	Dgkq	diacylglycerol kinase, theta	1,48	0,0321
1420860_at	Itga9	integrin alpha 9	1,48	0,0057
1437862_at	Rbm25	RNA binding motif protein 25	1,48	0,0136
1458637_x_at	NA	NA	1,48	0,0088
1422139_at	Plau	plasminogen activator, urokinase	1,48	0,0201
1441129_at	NA	NA	1,48	0,0323
1434998_at	Iqgap1	IQ motif containing GTPase activating protein 1	1,48	0,0033
1427418_a_at	Hif1a	hypoxia inducible factor 1, alpha subunit	1,48	0,0021
1448667_x_at	Tob2	transducer of ERBB2, 2	1,48	0,0411
1454422_at	4930456J16 Rik	RIKEN cDNA 4930456J16 gene	1,48	0,0081
1436181_at	Ddef2	development and differentiation enhancing factor 2	1,48	0,0407
1448299_at	Slc1a1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	1,48	0,0329
1438429_at	2610319H10 Rik	RIKEN cDNA 2610319H10 gene	1,48	0,0029

1416554_at	Pdlim1	PDZ and LIM domain 1 (elfin)	1,48	0,0257
1422219_a_at	Tbx20	T-box 20	1,48	0,0168
1426300_at	Alcam	activated leukocyte cell adhesion molecule	1,48	0,0038
1435938_at	Ckap2l	cytoskeleton associated protein 2-like	1,48	0,0447
1424483_at	Mobkl1b	MOB1, Mps One Binder kinase activator-like 1B (yeast)	1,48	0,0351
1423886_at	Lamc1	laminin, gamma 1	1,48	0,0142
1418261_at	Syk	spleen tyrosine kinase	1,48	0,0028
1439887_at	NA	NA	1,48	0,0380
1438168_x_at	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	1,48	0,0066
1434942_at	Esf1	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)	1,48	0,0043
1430521_s_at	Cpne8	copine VIII	1,48	0,0256
1441986_at	Zcchc6	zinc finger, CCHC domain containing 6	1,47	0,0110
1424755_at	Hip1	huntingtin interacting protein 1	1,47	0,0051
1425315_at	Dock7	dedicator of cytokinesis 7	1,47	0,0021
1456420_at	Arid4a	AT rich interactive domain 4A (RBP1-like)	1,47	0,0188
1437907_a_at	Tbca	tubulin cofactor A	1,47	0,0072
1458370_at	Bmp2k	BMP2 inducible kinase	1,47	0,0079
1429883_at	Actl6a	actin-like 6A	1,47	0,0156
1452108_at	Igf1r	insulin-like growth factor I receptor	1,47	0,0097
1445178_at	Sh3rf1	SH3 domain containing ring finger 1	1,47	0,0095
1415811_at	Uhrf1	ubiquitin-like, containing PHD and RING finger domains, 1	1,47	0,0440
1444361_at	Ap1s2	adaptor-related protein complex 1, sigma 2 subunit	1,47	0,0006
1426926_at	Plcg2	phospholipase C, gamma 2	1,47	0,0045
1419739_at	Tpm2	tropomyosin 2, beta	1,47	0,0183
1436985_at	Zfp644	zinc finger protein 644	1,47	0,0441
1452948_at	Tnfaip8l2	tumor necrosis factor, alpha-induced protein 8-like 2	1,47	0,0271
1444780_at	Nav2	neuron navigator 2	1,47	0,0335
1420330_at	Clec4e	C-type lectin domain family 4, member e	1,47	0,0272
1417756_a_at	Lsp1	lymphocyte specific 1	1,47	0,0443
1438312_s_at	Scyl1	SCY1-like 1 (S. cerevisiae)	1,46	0,0138
1418641_at	Lcp2	lymphocyte cytosolic protein 2	1,46	0,0302
1455900_x_at	Tgm2	transglutaminase 2, C polypeptide	1,46	0,0040
1422619_at	Ppap2a	phosphatidic acid phosphatase type 2A	1,46	0,0132
1424367_a_at	Homer2	homer homolog 2 (Drosophila)	1,46	0,0010
1423416_at	Smarcc1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	1,46	0,0165
1445728_at	Rdh18	retinol dehydrogenase 18	1,46	0,0432
1448919_at	Cd302	CD302 antigen	1,46	0,0088
1442075_at	AI314604	expressed sequence AI314604	1,46	0,0232
1449028_at	Rhou	ras homolog gene family, member U	1,46	0,0380
1429459_at	Sema3d	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D	1,46	0,0065
1429304_at	Ankrd10	ankyrin repeat domain 10	1,46	0,0018
1437020_at	Ep400	E1A binding protein p400	1,46	0,0198
1439901_at	NA	NA	1,46	0,0062
1452107_s_at	NA	NA	1,46	0,0442
1427299_at	Rps6ka3	ribosomal protein S6 kinase polypeptide 3	1,46	0,0058
1415856_at	Emb	embigin	1,46	0,0074
1427911_at	Tmem173	transmembrane protein 173	1,46	0,0040
1415919_at	Npdc1	neural proliferation, differentiation and control gene 1	1,46	0,0312
1428529_at	2810026P18 Rik	RIKEN cDNA 2810026P18 gene	1,46	0,0285
1420991_at	Ankrd1	ankyrin repeat domain 1 (cardiac muscle)	1,46	0,0194

1446946_at	NA	NA	1,46	0,0140
1447913_x_at	Akap9	A kinase (PRKA) anchor protein (yotiao) 9	1,45	0,0089
1443341_at	NA	NA	1,45	0,0436
1457664_x_at	C2	complement component 2 (within H-2S)	1,45	0,0491
1423725_at	Pls3	plastin 3 (T-isoform)	1,45	0,0143
1419610_at	Ccr1	chemokine (C-C motif) receptor 1	1,45	0,0036
1450851_at	Wdr1	WD repeat domain 1	1,45	0,0144
1436921_at	Atp7a	ATPase, Cu++ transporting, alpha polypeptide	1,45	0,0130
1423208_at	Tmem167	transmembrane protein 167	1,45	0,0105
1450541_at	Pvt1	plasmacytoma variant translocation 1	1,45	0,0151
1453313_at	Sesn3	sestrin 3	1,45	0,0212
1441486_at	Fkbp15	FK506 binding protein 15	1,45	0,0336
1420895_at	Tgfbr1	transforming growth factor, beta receptor I	1,45	0,0130
1425884_at	Bxdc1	brix domain containing 1	1,45	0,0267
1418591_at	Dnaja4	DnaJ (Hsp40) homolog, subfamily A, member 4	1,45	0,0038
1457233_at	Dnaja2	DnaJ (Hsp40) homolog, subfamily A, member 2	1,45	0,0170
1449353_at	Zmat3	zinc finger matrin type 3	1,45	0,0095
1430048_at	7630402I04Rik	RIKEN cDNA 7630402I04 gene	1,45	0,0402
1447931_at	Whsc1l1	Wolf-Hirschhorn syndrome candidate 1-like 1 (human)	1,45	0,0042
1435653_at	NA	NA	1,45	0,0071
1433776_at	Lhfp	lipoma HMGIC fusion partner	1,45	0,0023
1457753_at	Tlr13	toll-like receptor 13	1,45	0,0275
1425609_at	Ncf1	neutrophil cytosolic factor 1	1,45	0,0311
1440770_at	Bcl2	B-cell leukemia/lymphoma 2	1,45	0,0366
1417137_at	Uck2	uridine-cytidine kinase 2	1,45	0,0138
1454898_s_at	Iah1	isoamyl acetate-hydrolyzing esterase 1 homolog (S. cerevisiae)	1,45	0,0150
1438485_at	E130112L23Rik	RIKEN cDNA E130112L23 gene	1,45	0,0023
1438789_s_at	Dpysl3	dihydropyrimidinase-like 3	1,45	0,0186
1417455_at	Tgfb3	transforming growth factor, beta 3	1,44	0,0447
1437843_s_at	Nupl1	nucleoporin like 1	1,44	0,0414
1450099_a_at	Gba	glucosidase, beta, acid	1,44	0,0330
1439304_at	B230216N24Rik	RIKEN cDNA B230216N24 gene	1,44	0,0321
1428902_at	Chst11	carbohydrate sulfotransferase 11	1,44	0,0026
1452893_s_at	Enho	energy homeostasis associated	1,44	0,0357
1440167_s_at	Lpp	LIM domain containing preferred translocation partner in lipoma	1,44	0,0472
1423546_at	Zfp207	zinc finger protein 207	1,44	0,0015
1438730_at	BC028801	cDNA sequence BC028801	1,44	0,0114
1433964_s_at	Fermt3	fermitin family homolog 3 (Drosophila)	1,44	0,0131
1449840_at	Sntb2	syntrophin, basic 2	1,44	0,0033
1427266_at	Pbrm1	polybromo 1	1,44	0,0045
1437692_x_at	Anxa2	annexin A2	1,44	0,0210
1417380_at	Iqgap1	IQ motif containing GTPase activating protein 1	1,44	0,0192
1415704_a_at	Cdv3	carnitine deficiency-associated gene expressed in ventricle 3	1,44	0,0031
1427034_at	Ace	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	1,44	0,0452
1419208_at	Map3k8	mitogen-activated protein kinase kinase kinase 8	1,44	0,0343
1417124_at	Dstn	destrin	1,44	0,0144
1444235_at	1700025G04Rik	RIKEN cDNA 1700025G04 gene	1,44	0,0191
1424783_a_at	Ugt1a9	UDP glucuronosyltransferase 1 family, polypeptide	1,44	0,0115

		A9		
1442295_at	Arpc2	actin related protein 2/3 complex, subunit 2	1,44	0,0146
1422506_a_at	Cstb	cystatin B	1,44	0,0023
1439610_at	Rab27b	RAB27b, member RAS oncogene family	1,44	0,0029
1440414_at	Mtf1	metal response element binding transcription factor 1	1,44	0,0374
1442623_at	NA	NA	1,44	0,0032
1438531_at	A730054J21Rik	RIKEN cDNA A730054J21 gene	1,44	0,0324
1450083_at	Cnot4	CCR4-NOT transcription complex, subunit 4	1,44	0,0236
1422878_at	Syt12	synaptotagmin XII	1,44	0,0170
1416759_at	Mical1	microtubule associated monoxygenase, calponin and LIM domain containing 1	1,44	0,0162
1420398_at	Rgs18	regulator of G-protein signaling 18	1,44	0,0145
1428130_at	Lman1	lectin, mannose-binding, 1	1,44	0,0219
1460133_at	NA	NA	1,44	0,0026
1458616_at	NA	NA	1,44	0,0370
1429487_at	Ppp1r12a	protein phosphatase 1, regulatory (inhibitor) subunit 12A	1,44	0,0207
1460036_at	Ap1s2	adaptor-related protein complex 1, sigma 2 subunit	1,44	0,0294
1442845_at	C130075A20Rik	RIKEN cDNA C130075A20 gene	1,43	0,0070
1421905_at	Tgs1	trimethylguanosine synthase homolog (S. cerevisiae)	1,43	0,0307
1440092_at	NA	NA	1,43	0,0117
1435875_at	Prkab2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	1,43	0,0043
1445311_at	Akap13	A kinase (PRKA) anchor protein 13	1,43	0,0397
1434458_at	Fst	follistatin	1,43	0,0091
1447984_at	D1Ertd75e	DNA segment, Chr 1, ERATO Doi 75, expressed	1,43	0,0415
1451418_a_at	Spsb4	splA/ryanodine receptor domain and SOCS box containing 4	1,43	0,0378
1448950_at	Il1r1	interleukin 1 receptor, type I	1,43	0,0106
1441204_at	A130019P10Rik	RIKEN cDNA A130019P10 gene	1,43	0,0044
1420980_at	Pak1	p21 (CDKN1A)-activated kinase 1	1,43	0,0052
1437821_at	NA	NA	1,43	0,0053
1452784_at	Itgav	integrin alpha V	1,43	0,0096
1452381_at	Creb3l2	cAMP responsive element binding protein 3-like 2	1,43	0,0140
1429659_at	Smc2	structural maintenance of chromosomes 2	1,43	0,0245
1433581_at	1190002N15Rik	RIKEN cDNA 1190002N15 gene	1,43	0,0388
1418110_a_at	Inpp5d	inositol polyphosphate-5-phosphatase D	1,43	0,0107
1417135_at	Srpk2	serine/arginine-rich protein specific kinase 2	1,43	0,0315
1426612_at	Tipin	timeless interacting protein	1,43	0,0037
1444701_at	Mex3c	mex3 homolog C (C. elegans)	1,43	0,0100
1441968_at	Tspan9	tetraspanin 9	1,43	0,0191
1415827_a_at	Serp1	stress-associated endoplasmic reticulum protein 1	1,43	0,0246
1429478_at	6720463M24Rik	RIKEN cDNA 6720463M24 gene	1,43	0,0438
1426941_at	Muc15	mucin 15	1,43	0,0161
1444570_at	NA	NA	1,43	0,0152
1417040_a_at	Bok	BCL2-related ovarian killer protein	1,43	0,0392
1421223_a_at	Anxa4	annexin A4	1,43	0,0032
1422195_s_at	Tbx15	T-box 15	1,43	0,0190
1452280_at	Farp1	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-derived)	1,42	0,0010
1446938_at	AA408213	expressed sequence AA408213	1,42	0,0165
1426370_at	Far1	fatty acyl CoA reductase 1	1,42	0,0091

1425850_a_at	Nek6	NIMA (never in mitosis gene a)-related expressed kinase 6	1,42	0,0161
1419695_at	St8sia1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	1,42	0,0399
1440011_at	NA	NA	1,42	0,0313
1456826_at	Taok2	TAO kinase 2	1,42	0,0274
1419236_at	Helb	helicase (DNA) B	1,42	0,0459
1451832_at	Cklf	chemokine-like factor	1,42	0,0315
1456653_a_at	Mthfd1l	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	1,42	0,0252
1423596_at	Nek6	NIMA (never in mitosis gene a)-related expressed kinase 6	1,42	0,0117
1450658_at	Adamts5	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2)	1,42	0,0357
1456893_at	NA	NA	1,42	0,0178
1437635_at	St3gal6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	1,42	0,0017
1439413_x_at	Morf4l2	mortality factor 4 like 2	1,42	0,0041
1416066_at	Cd9	CD9 antigen	1,42	0,0047
1452769_at	Rnf145	ring finger protein 145	1,42	0,0030
1423875_at	Fam160b1	family with sequence similarity 160, member B1	1,42	0,0178
1457088_at	Pldn	pallidin	1,42	0,0402
1428168_at	Mpzl1	myelin protein zero-like 1	1,42	0,0417
1456743_x_at	Morf4l2	mortality factor 4 like 2	1,42	0,0041
1426534_a_at	Arfgap3	ADP-ribosylation factor GTPase activating protein 3	1,42	0,0040
1421253_at	Nrap	nebulin-related anchoring protein	1,42	0,0041
1460243_at	Sptlc2	serine palmitoyltransferase, long chain base subunit 2	1,42	0,0245
1436171_at	Arhgap30	Rho GTPase activating protein 30	1,41	0,0405
1424424_at	Slc39a1	solute carrier family 39 (zinc transporter), member 1	1,41	0,0064
1446326_at	Col1a2	collagen, type I, alpha 2	1,41	0,0475
1418429_at	Kif5b	kinesin family member 5B	1,41	0,0133
1416548_at	Slc35b4	solute carrier family 35, member B4	1,41	0,0181
1444241_at	LOC100044766	similar to WW domain-containing adapter protein with coiled-coil	1,41	0,0130
1444483_at	NA	NA	1,41	0,0372
1441243_at	NA	NA	1,41	0,0053
1431311_at	NA	NA	1,41	0,0151
1445066_at	NA	NA	1,41	0,0156
1444006_at	Setd2	SET domain containing 2	1,41	0,0323
1448885_at	Rap2b	RAP2B, member of RAS oncogene family	1,41	0,0136
1429270_a_at	Syce2	synaptonemal complex central element protein 2	1,41	0,0345
1447143_at	NA	NA	1,41	0,0443
1424894_at	Rab13	RAB13, member RAS oncogene family	1,41	0,0401
1454950_at	Fam168a	family with sequence similarity 168, member A	1,41	0,0339
1445252_at	Kremen1	kringle containing transmembrane protein 1	1,41	0,0235
1442331_at	NA	NA	1,41	0,0122
1442347_at	Lrp8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	1,41	0,0391
1455994_x_at	Elovl1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	1,41	0,0230
1447426_at	NA	NA	1,41	0,0389
1451419_at	Spsb4	splA/ryanodine receptor domain and SOCS box containing 4	1,41	0,0440
1453015_at	5830471E12Rik	RIKEN cDNA 5830471E12 gene	1,41	0,0073
1440247_at	Phf14	PHD finger protein 14	1,41	0,0039
1460526_at	4833420L08	RIKEN cDNA 4833420L08 gene	1,41	0,0175

	Rik			
1444886_at	NA	NA	1,41	0,0469
1433481_at	Fkbp14	FK506 binding protein 14	1,41	0,0109
1456382_at	Atad1	ATPase family, AAA domain containing 1	1,41	0,0321
1428136_at	Sfrp1	secreted frizzled-related protein 1	1,41	0,0461
1419898_s_at	Zc3h7a	zinc finger CCCH type containing 7 A	1,41	0,0187
1426392_a_at	Actr3	ARP3 actin-related protein 3 homolog (yeast)	1,41	0,0111
1437467_at	Alcam	activated leukocyte cell adhesion molecule	1,41	0,0329
1433467_at	Slc7a6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	1,41	0,0028
1426603_at	Rnasel	ribonuclease L (2', 5'-oligoisoadenylate synthetase-dependent)	1,41	0,0047
1426559_at	Sbno1	sno, strawberry notch homolog 1 (Drosophila)	1,40	0,0151
1442951_at	NA	NA	1,40	0,0185
1443090_at	NA	NA	1,40	0,0446
1448954_at	Nrip3	nuclear receptor interacting protein 3	1,40	0,0468
1457706_at	BC030336	cDNA sequence BC030336	1,40	0,0323
1459332_at	Itch	itchy, E3 ubiquitin protein ligase	1,40	0,0289
1454780_at	Galntl4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4	1,40	0,0154
1424110_a_at	Nme1	non-metastatic cells 1, protein (NM23A) expressed in	1,40	0,0095
1455656_at	Btla	B and T lymphocyte associated	1,40	0,0141
1451100_a_at	Cdv3	carnitine deficiency-associated gene expressed in ventricle 3	1,40	0,0087
1427169_at	Pard3b	par-3 partitioning defective 3 homolog B (C. elegans)	1,40	0,0050
1451319_at	Senp1	SUMO1/sentrin specific peptidase 1	1,40	0,0173
1460104_at	Vps4b	vacuolar protein sorting 4b (yeast)	1,40	0,0329
1443330_at	D1Ertd646e	DNA segment, Chr 1, ERATO Doi 646, expressed	1,40	0,0264
1419829_a_at	NA	NA	1,40	0,0087
1458886_at	NA	NA	1,40	0,0247
1418895_at	Skap2	src family associated phosphoprotein 2	1,40	0,0294
1456611_at	Fam13a	family with sequence similarity 13, member A	1,40	0,0387
1444273_at	AW555355	expressed sequence AW555355	1,40	0,0207
1424198_at	Dlg5	discs, large homolog 5 (Drosophila)	1,40	0,0136
1449265_at	Casp1	caspase 1	1,40	0,0201
1428983_at	Scx	scleraxis	1,40	0,0199
1438437_a_at	4933439C10Rik	RIKEN cDNA 4933439C10 gene	1,40	0,0313
1421654_a_at	Lmna	lamin A	1,40	0,0047
1437886_at	Klhl6	kelch-like 6 (Drosophila)	1,40	0,0440
1426477_at	Rasa1	RAS p21 protein activator 1	1,40	0,0323
1433505_a_at	Lrrc8d	leucine rich repeat containing 8D	1,40	0,0053
1436546_at	NA	NA	1,40	0,0304
1426951_at	Crim1	cysteine rich transmembrane BMP regulator 1 (chordin like)	1,40	0,0355
1458884_at	Plekha1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	1,40	0,0296
1456294_at	Rnft1	ring finger protein, transmembrane 1	1,39	0,0422
1444229_at	Nr2f2	nuclear receptor subfamily 2, group F, member 2	1,39	0,0126
1446807_at	Usp50	ubiquitin specific peptidase 50	1,39	0,0346
1458988_at	NA	NA	1,39	0,0264
1417068_a_at	Ptpn1	protein tyrosine phosphatase, non-receptor type 1	1,39	0,0038
1424529_s_at	Cgref1	cell growth regulator with EF hand domain 1	1,39	0,0241
1431831_at	2210009G21Rik	RIKEN cDNA 2210009G21 gene	1,39	0,0178
1442050_at	Zfp608	zinc finger protein 608	1,39	0,0264
1423956_at	Smap1	stromal membrane-associated protein 1	1,39	0,0058

1422550_a_at	Mtap6	microtubule-associated protein 6	1,39	0,0115
1457782_at	Tln1	talin 1	1,39	0,0255
1425460_at	Mtmr2	myotubularin related protein 2	1,39	0,0198
1451649_a_at	Wdr75	WD repeat domain 75	1,39	0,0116
1437864_at	Adipor2	adiponectin receptor 2	1,39	0,0302
1418981_at	Casp12	caspase 12	1,39	0,0371
1444101_at	Odf2	outer dense fiber of sperm tails 2	1,39	0,0193
1433831_at	4833418A01 Rik	RIKEN cDNA 4833418A01 gene	1,39	0,0442
1439209_at	Tcf12	transcription factor 12	1,39	0,0091
1448513_a_at	Npc2	Niemann Pick type C2	1,39	0,0040
1454664_a_at	Eif5	eukaryotic translation initiation factor 5	1,39	0,0493
1435517_x_at	Ralb	v-ral simian leukemia viral oncogene homolog B (ras related)	1,39	0,0088
1456503_at	Nup214	nucleoporin 214	1,39	0,0284
1424987_at	5430435G22Rik	RIKEN cDNA 5430435G22 gene	1,39	0,0088
1423465_at	Frrs1	ferric-chelate reductase 1	1,39	0,0171
1446361_at	NA	NA	1,39	0,0183
1442550_at	NA	NA	1,39	0,0168
1452839_at	Dph5	DPH5 homolog (S. cerevisiae)	1,39	0,0177
1451362_at	Rab7l1	RAB7, member RAS oncogene family-like 1	1,39	0,0189
1422286_a_at	Tgif1	TGFB-induced factor homeobox 1	1,39	0,0342
1443314_at	Slc12a6	solute carrier family 12, member 6	1,39	0,0338
1418822_a_at	Arf6	ADP-ribosylation factor 6	1,39	0,0402
1426329_s_at	Baalc	brain and acute leukemia, cytoplasmic	1,39	0,0383
1417012_at	Sdc2	syndecan 2	1,39	0,0308
1441660_at	Actr2	ARP2 actin-related protein 2 homolog (yeast)	1,39	0,0480
1433531_at	Acsl4	acyl-CoA synthetase long-chain family member 4	1,39	0,0483
1437333_x_at	Aldh18a1	aldehyde dehydrogenase 18 family, member A1	1,39	0,0360
1437277_x_at	Tgm2	transglutaminase 2, C polypeptide	1,39	0,0087
1433412_at	Fam108b	family with sequence similarity 108, member B	1,39	0,0177
1421413_a_at	Pdlim5	PDZ and LIM domain 5	1,39	0,0312
1460671_at	Gpx1	glutathione peroxidase 1	1,38	0,0028
1422812_at	Cxcr6	chemokine (C-X-C motif) receptor 6	1,38	0,0032
1422733_at	Fjx1	four jointed box 1 (Drosophila)	1,38	0,0086
1416094_at	Adam9	a disintegrin and metallopeptidase domain 9 (meltrin gamma)	1,38	0,0008
1444796_at	C76876	expressed sequence C76876	1,38	0,0131
1456720_at	NA	NA	1,38	0,0361
1447345_at	NA	NA	1,38	0,0081
1416606_s_at	Nhp2	NHP2 ribonucleoprotein homolog (yeast)	1,38	0,0037
1449530_at	Trps1	trichorhinophalangeal syndrome I (human)	1,38	0,0057
1426461_at	Ugp2	UDP-glucose pyrophosphorylase 2	1,38	0,0029
1441052_at	NA	NA	1,38	0,0154
1460338_a_at	Crlf3	cytokine receptor-like factor 3	1,38	0,0053
1424832_at	4732429D16 Rik	RIKEN cDNA 4732429D16 gene	1,38	0,0324
1434951_at	Armc8	armadillo repeat containing 8	1,38	0,0414
1459253_at	Arrdc3	arrestin domain containing 3	1,38	0,0445
1449859_at	Golt1b	golgi transport 1 homolog B (S. cerevisiae)	1,38	0,0234
1460287_at	Timp2	tissue inhibitor of metalloproteinase 2	1,38	0,0457
1445440_at	Ccdc88a	coiled coil domain containing 88A	1,38	0,0066
1440559_at	Hmga2-ps1	high mobility group AT-hook 2, pseudogene 1	1,38	0,0454
1416527_at	Rab32	RAB32, member RAS oncogene family	1,38	0,0242
1426903_at	Fndc3a	fibronectin type III domain containing 3A	1,38	0,0274

1450291_s_at	Ms4a4c	membrane-spanning 4-domains, subfamily A, member 4C	1,38	0,0078
1434949_at	Armc8	armadillo repeat containing 8	1,38	0,0482
1442849_at	Lrp1	low density lipoprotein receptor-related protein 1	1,38	0,0072
1446850_at	NA	NA	1,38	0,0179
1451154_a_at	Cugbp2	CUG triplet repeat, RNA binding protein 2	1,38	0,0101
1440920_at	Mmp14	matrix metallopeptidase 14 (membrane-inserted)	1,37	0,0047
1433820_a_at	1110012D08 Rik	RIKEN cDNA 1110012D08 gene	1,37	0,0281
1447985_s_at	Ankib1	ankyrin repeat and IBR domain containing 1	1,37	0,0414
1434519_at	Ddah1	dimethylarginine dimethylaminohydrolase 1	1,37	0,0228
1451316_a_at	Picalm	phosphatidylinositol binding clathrin assembly protein	1,37	0,0366
1422053_at	Inhba	inhibin beta-A	1,37	0,0198
1416002_x_at	Cotl1	coactosin-like 1 (Dictyostelium)	1,37	0,0433
1426081_a_at	Dio2	deiodinase, iodothyronine, type II	1,37	0,0254
1443654_at	Ankfy1	ankyrin repeat and FYVE domain containing 1	1,37	0,0459
1445105_at	NA	NA	1,37	0,0450
1454724_x_at	Fam108b	family with sequence similarity 108, member B	1,37	0,0456
1459865_x_at	Ces7	carboxylesterase 7	1,37	0,0131
1425523_at	Rbm25	RNA binding motif protein 25	1,37	0,0295
1455040_s_at	RP23-448C18.1	novel similar to human Nance-Horan syndrome protein (RP11-262D11.5)	1,37	0,0473
1431361_at	Prcp	prolylcarboxypeptidase (angiotensinase C)	1,37	0,0101
1436293_x_at	Ildr2	immunoglobulin-like domain containing receptor 2	1,37	0,0110
1447280_at	NA	NA	1,37	0,0477
1438663_at	Bat2d	BAT2 domain containing 1	1,37	0,0293
1439044_at	Zfp354c	zinc finger protein 354C	1,37	0,0400
1419728_at	Cxcl5	chemokine (C-X-C motif) ligand 5	1,37	0,0030
1439318_at	Mast4	microtubule associated serine/threonine kinase family member 4	1,37	0,0243
1446490_at	NA	NA	1,37	0,0252
1436938_at	Rbms3	RNA binding motif, single stranded interacting protein	1,37	0,0393
1417884_at	Slc16a6	solute carrier family 16 (monocarboxylic acid transporters), member 6	1,37	0,0389
1460541_at	Slc7a6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	1,37	0,0310
1452374_at	Zfp322a	zinc finger protein 322A	1,37	0,0076
1420957_at	Apc	adenomatosis polyposis coli	1,37	0,0166
1420992_at	Ankrd1	ankyrin repeat domain 1 (cardiac muscle)	1,36	0,0130
1452051_at	Actr3	ARP3 actin-related protein 3 homolog (yeast)	1,36	0,0196
1455960_at	Megf9	multiple EGF-like-domains 9	1,36	0,0412
1456887_at	Cmklr1	chemokine-like receptor 1	1,36	0,0192
1455016_at	Prpf38b	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	1,36	0,0493
1459801_at	B3galt5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	1,36	0,0135
1427854_x_at	Hspb1	heat shock protein 1	1,36	0,0312
1449042_at	Ctcf	CCCTC-binding factor	1,36	0,0491
1439432_x_at	Morf4l2	mortality factor 4 like 2	1,36	0,0161
1432719_at	4833412K13 Rik	RIKEN cDNA 4833412K13 gene	1,36	0,0083
1448283_a_at	Uba2	ubiquitin-like modifier activating enzyme 2	1,36	0,0046
1426812_a_at	Fam129b	family with sequence similarity 129, member B	1,36	0,0495
1444232_at	Prkg1	protein kinase, cGMP-dependent, type I	1,36	0,0094
1455580_at	Usp6nl	USP6 N-terminal like	1,36	0,0444
1419867_a_at	Ankhd1	ankyrin repeat and KH domain containing 1	1,36	0,0442
1433440_x_at	Uba2	ubiquitin-like modifier activating enzyme 2	1,36	0,0118

1457814_at	NA	NA	1,36	0,0485
1429400_at	Clcn5	chloride channel 5	1,36	0,0015
1445826_at	Ankrd17	ankyrin repeat domain 17	1,36	0,0279
1449947_s_at	Zfhx3	zinc finger homeobox 3	1,36	0,0158
1421385_a_at	Myo7a	myosin VIIA	1,36	0,0151
1418324_at	Fem1b	feminization 1 homolog b (C. elegans)	1,36	0,0336
1426587_a_at	Stat3	signal transducer and activator of transcription 3	1,36	0,0459
1417291_at	Tnfrsf1a	tumor necrosis factor receptor superfamily, member 1a	1,36	0,0005
1434975_x_at	4933439C20 Rik	RIKEN cDNA 4933439C20 gene	1,36	0,0447
1446434_at	NA	NA	1,36	0,0030
1416844_at	Prmt2	protein arginine N-methyltransferase 2	1,36	0,0148
1439394_x_at	Cdc20	cell division cycle 20 homolog (S. cerevisiae)	1,36	0,0290
1451985_at	Lrrk1	leucine-rich repeat kinase 1	1,36	0,0192
1451750_at	Irak4	interleukin-1 receptor-associated kinase 4	1,36	0,0072
1433547_s_at	Nudcd1	NudC domain containing 1	1,36	0,0288
1421792_s_at	Trem2	triggering receptor expressed on myeloid cells 2	1,36	0,0256
1447509_at	NA	NA	1,36	0,0336
1447594_at	1810012K16 Rik	RIKEN cDNA 1810012K16 gene	1,36	0,0253
1417774_at	Nans	N-acetylneuraminic acid synthase (sialic acid synthase)	1,36	0,0370
1457211_at	Gls	glutaminase	1,35	0,0009
1443651_at	Phc3	polyhomeotic-like 3 (Drosophila)	1,35	0,0018
1419250_a_at	Pftk1	PFTAIRE protein kinase 1	1,35	0,0025
1431432_at	Cfl2	cofilin 2, muscle	1,35	0,0171
1419806_at	Hdlbp	high density lipoprotein (HDL) binding protein	1,35	0,0339
1453796_a_at	Ergic2	ERGIC and golgi 2	1,35	0,0234
1450959_at	D930014E17Rik	RIKEN cDNA D930014E17 gene	1,35	0,0048
1429963_at	Mapk6	mitogen-activated protein kinase 6	1,35	0,0322
1424940_s_at	BC022687	cDNA sequence BC022687	1,35	0,0236
1418539_a_at	Ptpre	protein tyrosine phosphatase, receptor type, E	1,35	0,0076
1436063_at	Loxl1	lysyl oxidase-like 1	1,35	0,0242
1455642_a_at	Tspan17	tetraspanin 17	1,35	0,0095
1456205_x_at	Tbca	tubulin cofactor A	1,35	0,0044
1420023_at	Etf1	eukaryotic translation termination factor 1	1,35	0,0306
1416108_a_at	Tmed3	transmembrane emp24 domain containing 3	1,35	0,0078
1421326_at	Csf2rb	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	1,35	0,0447
1429549_at	Col27a1	collagen, type XXVII, alpha 1	1,35	0,0087
1437392_at	OTTMUSG00000015750	predicted gene, OTTMUSG00000015750	1,35	0,0302
1417719_at	Sap30	sin3 associated polypeptide	1,35	0,0118
1416189_a_at	Sec61a1	Sec61 alpha 1 subunit (S. cerevisiae)	1,35	0,0055
1416311_s_at	Tuba3a	tubulin, alpha 3A	1,35	0,0479
1428156_at	Gng2	guanine nucleotide binding protein (G protein), gamma 2	1,35	0,0269
1437526_x_at	EG620521	predicted gene, EG620521	1,35	0,0478
1458057_at	NA	NA	1,35	0,0378
1419108_at	Ophn1	oligophrenin 1	1,35	0,0108
1446444_at	Rc3h2	ring finger and CCCH-type zinc finger domains 2	1,35	0,0417
1424912_at	Slc25a17	solute carrier family 25 (mitochondrial carrier, peroxisomal membrane protein), member 17	1,35	0,0285
1433428_x_at	Tgm2	transglutaminase 2, C polypeptide	1,35	0,0146
1456712_at	Lcorl	ligand dependent nuclear receptor corepressor-like	1,35	0,0142

1420935_a_at	Srrm1	serine/arginine repetitive matrix 1	1,35	0,0132
1416598_at	Glis2	GLIS family zinc finger 2	1,35	0,0453
1447567_at	Odz3	odd Oz/ten-m homolog 3 (Drosophila)	1,35	0,0187
1456196_x_at	Fkbp1a	FK506 binding protein 1a	1,35	0,0044
1451218_at	Edem1	ER degradation enhancer, mannosidase alpha-like 1	1,35	0,0472
1437632_at	Med14	mediator complex subunit 14	1,35	0,0389
1418379_s_at	Gpr124	G protein-coupled receptor 124	1,34	0,0193
1433908_a_at	Cttn	cortactin	1,34	0,0013
1446351_at	D430034N21	hypothetical protein D430034N21	1,34	0,0040
1449968_s_at	Acot10	acyl-CoA thioesterase 10	1,34	0,0019
1447685_x_at	Ets2	E26 avian leukemia oncogene 2, 3' domain	1,34	0,0483
1433962_at	Trmt61a	tRNA methyltransferase 61 homolog A (S. cerevisiae)	1,34	0,0190
1458134_at	NA	NA	1,34	0,0194
1448378_at	Fscn1	fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratus)	1,34	0,0137
1458073_at	9330156P08Rik	RIKEN cDNA 9330156P08 gene	1,34	0,0397
1459847_x_at	Gfra2	glial cell line derived neurotrophic factor family receptor alpha 2	1,34	0,0201
1438508_at	NA	NA	1,34	0,0475
1423521_at	Lmnb1	lamin B1	1,34	0,0487
1420818_at	Sla	src-like adaptor	1,34	0,0207
1455649_at	Ttc9	tetratricopeptide repeat domain 9	1,34	0,0147
1423484_at	Bicc1	bicaudal C homolog 1 (Drosophila)	1,34	0,0233
1436311_at	Gemin5	gem (nuclear organelle) associated protein 5	1,34	0,0424
1440404_at	NA	NA	1,34	0,0147
1430151_at	Nisch	nischarin	1,34	0,0482
1444677_at	C77673	expressed sequence C77673	1,34	0,0298
1451643_a_at	Rab4b	RAB4B, member RAS oncogene family	1,34	0,0174
1449209_a_at	Rdh11	retinol dehydrogenase 11	1,34	0,0326
1442523_at	EG331392	predicted gene, EG331392	1,34	0,0208
1424398_at	Dhx36	DEAH (Asp-Glu-Ala-His) box polypeptide 36	1,34	0,0207
1417995_at	Ptpn22	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	1,34	0,0172
1428325_at	Cnpy4	canopy 4 homolog (zebrafish)	1,34	0,0389
1448148_at	Grn	granulin	1,34	0,0143
1446737_a_at	Hook3	hook homolog 3 (Drosophila)	1,34	0,0231
1432787_at	6720420G18Rik	RIKEN cDNA 6720420G18 gene	1,34	0,0313
1417319_at	Pvrl3	poliovirus receptor-related 3	1,34	0,0488
1417417_a_at	Cox6a1	cytochrome c oxidase, subunit VI a, polypeptide 1	1,34	0,0254
1456530_x_at	Elovl1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	1,34	0,0479
1429937_at	Utp23	UTP23, small subunit (SSU) processome component, homolog (yeast)	1,34	0,0026
1455833_at	Afap1l2	actin filament associated protein 1-like 2	1,34	0,0252
1433502_s_at	Tsr1	TSR1, 20S rRNA accumulation, homolog (yeast)	1,34	0,0184
1433833_at	Fndc3b	fibronectin type III domain containing 3B	1,34	0,0495
1424084_at	Rod1	ROD1 regulator of differentiation 1 (S. pombe)	1,34	0,0038
1452451_at	mCG_21548	brain expressed, associated with Nedd4	1,34	0,0137
1417471_s_at	D1Ertd622e	DNA segment, Chr 1, ERATO Doi 622, expressed	1,34	0,0482
1449278_at	Eif2ak3	eukaryotic translation initiation factor 2 alpha kinase 3	1,33	0,0281
1418998_at	Kmo	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	1,33	0,0121
1424389_at	Nupl1	nucleoporin like 1	1,33	0,0313
1447272_s_at	Atp10a	ATPase, class V, type 10A	1,33	0,0109

1426976_at	Usp47	ubiquitin specific peptidase 47	1,33	0,0077
1444320_at	Ddhd2	DDHD domain containing 2	1,33	0,0426
1416489_at	Pi4k2b	phosphatidylinositol 4-kinase type 2 beta	1,33	0,0340
1453228_at	Stx11	syntaxin 11	1,33	0,0440
1446289_at	NA	NA	1,33	0,0117
1437148_at	Arpc2	actin related protein 2/3 complex, subunit 2	1,33	0,0015
1457615_at	NA	NA	1,33	0,0048
1431099_at	Hoxd8	homeo box D8	1,33	0,0230
1449323_a_at	Rpl3	ribosomal protein L3	1,33	0,0011
1435136_at	Whsc1	Wolf-Hirschhorn syndrome candidate 1 (human)	1,33	0,0173
1442116_at	Gpr176	G protein-coupled receptor 176	1,33	0,0272
1455489_at	Lrrtm2	leucine rich repeat transmembrane neuronal 2	1,33	0,0437
1431462_at	Ppp1r12b	protein phosphatase 1, regulatory (inhibitor) subunit 12B	1,33	0,0083
1457569_at	D8Ertd51e	DNA segment, Chr 8, ERATO Doi 51, expressed	1,33	0,0159
1457770_at	Slc39a14	solute carrier family 39 (zinc transporter), member 14	1,33	0,0304
1438621_x_at	Axl	AXL receptor tyrosine kinase	1,33	0,0494
1457935_at	NA	NA	1,33	0,0264
1418963_at	2310047O13Rik	RIKEN cDNA 2310047O13 gene	1,33	0,0058
1419061_at	Rhod	ras homolog gene family, member D	1,33	0,0366
1447781_s_at	Rg9mtd2	RNA (guanine-9-) methyltransferase domain containing 2	1,33	0,0292
1420473_at	Mtpn	myotrophin	1,33	0,0130
1452415_at	Actn1	actinin, alpha 1	1,33	0,0264
1437465_a_at	P4hb	prolyl 4-hydroxylase, beta polypeptide	1,33	0,0105
1458054_at	Ext1	exostoses (multiple) 1	1,33	0,0275
1443303_at	NA	NA	1,33	0,0245
1448250_at	9030425E11Rik	RIKEN cDNA 9030425E11 gene	1,33	0,0232
1418075_at	St6galnac4	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4	1,33	0,0426
1416028_a_at	Hn1	hematological and neurological expressed sequence 1	1,33	0,0264
1438771_at	Brd1	bromodomain containing 1	1,33	0,0324
1436660_at	Rrbp1	ribosome binding protein 1	1,33	0,0477
1460437_at	Cyth4	cytohesin 4	1,33	0,0295
1448409_at	Lrmp	lymphoid-restricted membrane protein	1,33	0,0200
1459622_at	Gm22	gene model 22, (NCBI)	1,33	0,0267
1423643_at	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	1,32	0,0309
1437618_x_at	Gpr85	G protein-coupled receptor 85	1,32	0,0088
1441396_at	B3galt1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	1,32	0,0040
1423877_at	Chaf1b	chromatin assembly factor 1, subunit B (p60)	1,32	0,0438
1446941_at	C78505	expressed sequence C78505	1,32	0,0061
1436900_x_at	Leprot	leptin receptor overlapping transcript	1,32	0,0211
1428373_at	Ip6k2	inositol hexaphosphate kinase 2	1,32	0,0307
1455799_at	Rorb	RAR-related orphan receptor beta	1,32	0,0478
1416901_at	Npc2	Niemann Pick type C2	1,32	0,0061
1426569_a_at	Frk	fyn-related kinase	1,32	0,0452
1426685_a_at	Cnot6	CCR4-NOT transcription complex, subunit 6	1,32	0,0440
1447549_x_at	Ninj1	ninjurin 1	1,32	0,0192
1446209_at	Usp40	ubiquitin specific peptidase 40	1,32	0,0133
1427229_at	Hmgcr	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	1,32	0,0491
1419648_at	Myo1c	myosin IC	1,32	0,0249
1434590_at	Bend6	BEN domain containing 6	1,32	0,0145

1438947_x_at	Sema3f	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	1,32	0,0303
1426573_at	Me2	malic enzyme 2, NAD(+)-dependent, mitochondrial	1,32	0,0447
1444931_at	NA	NA	1,32	0,0498
1427231_at	Robo1	roundabout homolog 1 (Drosophila)	1,32	0,0466
1418545_at	Wasf1	WASP family 1	1,32	0,0243
1450911_at	Ppib	peptidylprolyl isomerase B	1,32	0,0048
1456488_at	Wdr33	WD repeat domain 33	1,32	0,0295
1450964_a_at	Osbpl9	oxysterol binding protein-like 9	1,32	0,0054
1441632_at	C130079B09Rik	RIKEN cDNA C130079B09 gene	1,32	0,0448
1445966_at	NA	NA	1,32	0,0076
1434985_a_at	Eif4a1	eukaryotic translation initiation factor 4A1	1,31	0,0059
1415778_at	Morf4l2	mortality factor 4 like 2	1,31	0,0054
1422593_at	Ap3s1	adaptor-related protein complex 3, sigma 1 subunit	1,31	0,0224
1443222_at	NA	NA	1,31	0,0328
1418305_s_at	Gar1	GAR1 ribonucleoprotein homolog (yeast)	1,31	0,0220
1451120_at	Polr1d	polymerase (RNA) I polypeptide D	1,31	0,0157
1450018_s_at	Slc25a30	solute carrier family 25, member 30	1,31	0,0449
1437615_s_at	Vps37c	vacuolar protein sorting 37C (yeast)	1,31	0,0256
1455725_a_at	LOC100045490	similar to H3 histone, family 3A	1,31	0,0231
1418512_at	Stk3	serine/threonine kinase 3 (Ste20, yeast homolog)	1,31	0,0267
1430918_at	Mrz 03	membrane-associated ring finger (C3HC4) 3	1,31	0,0141
1434959_at	Dhh	desert hedgehog	1,31	0,0070
1416308_at	Ugdh	UDP-glucose dehydrogenase	1,31	0,0245
1454060_a_at	Nras	neuroblastoma ras oncogene	1,31	0,0493
1452286_at	Slain2	SLAIN motif family, member 2	1,31	0,0009
1447703_x_at	Zfp593	zinc finger protein 593	1,31	0,0495
1417523_at	Plek	pleckstrin	1,31	0,0076
1441750_x_at	4930447F24Rik	RIKEN cDNA 4930447F24 gene	1,31	0,0288
1459254_at	Cdca2	cell division cycle associated 2	1,31	0,0142
1436497_at	NA	NA	1,31	0,0231
1415944_at	Sdc1	syndecan 1	1,31	0,0152
1429671_at	Scand3	SCAN domain containing 3	1,31	0,0197
1444562_at	NA	NA	1,31	0,0095
1446653_at	NA	NA	1,31	0,0283
1453448_at	2310067E19Rik	RIKEN cDNA 2310067E19 gene	1,31	0,0491
1422629_s_at	Shroom3	shroom family member 3	1,31	0,0445
1446670_at	NA	NA	1,31	0,0430
1436332_at	Hspb6	heat shock protein, alpha-crystallin-related, B6	1,30	0,0030
1446972_at	D15Wsu126e	DNA segment, Chr 15, Wayne State University 126, expressed	1,30	0,0123
1416744_at	Uap1	UDP-N-acetylglucosamine pyrophosphorylase 1	1,30	0,0475
1420613_at	Ptp4a2	protein tyrosine phosphatase 4a2	1,30	0,0414
1448180_a_at	Hn1	hematological and neurological expressed sequence 1	1,30	0,0112
1434158_at	Gmds	GDP-mannose 4, 6-dehydratase	1,30	0,0178
1439060_s_at	Wipi1	WD repeat domain, phosphoinositide interacting 1	1,30	0,0043
1423383_a_at	Osbpl9	oxysterol binding protein-like 9	1,30	0,0069
1452410_a_at	Fes	feline sarcoma oncogene	1,30	0,0414
1437074_at	Snx5	sorting nexin 5	1,30	0,0495
1428527_at	Snx7	sorting nexin 7	1,30	0,0057
1446570_at	NA	NA	1,30	0,0178

1455731_at	Slc29a3	solute carrier family 29 (nucleoside transporters), member 3	1,30	0,0281
1427143_at	Jarid1b	jumonji, AT rich interactive domain 1B (Rbp2 like)	1,30	0,0067
1439814_at	Atp8b4	ATPase, class I, type 8B, member 4	1,30	0,0494
1425921_a_at	1810055G02Rik	RIKEN cDNA 1810055G02 gene	1,30	0,0296
1426854_a_at	LOC100047898	similar to protein phosphatase 2A inhibitor-2 I-2PP2A	1,30	0,0442
1459011_at	NA	NA	1,30	0,0460
1434968_a_at	Actr3	ARP3 actin-related protein 3 homolog (yeast)	1,30	0,0034
1420649_at	Zfhx3	zinc finger homeobox 3	1,30	0,0128
1424134_at	Rspry1	ring finger and SPRY domain containing 1	1,30	0,0048
1457434_s_at	Ptpla	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a	1,30	0,0075
1451798_at	Il1rn	interleukin 1 receptor antagonist	1,30	0,0428
1437735_at	Ppp1r12a	protein phosphatase 1, regulatory (inhibitor) subunit 12A	1,30	0,0443
1449258_at	D11Wsu99e	DNA segment, Chr 11, Wayne State University 99, expressed	1,30	0,0037
1434087_at	Mthfr	5,10-methylenetetrahydrofolate reductase	1,30	0,0114
1434485_a_at	Ugp2	UDP-glucose pyrophosphorylase 2	1,30	0,0413
1442590_at	Tnfrsf22	tumor necrosis factor receptor superfamily, member 22	1,30	0,0406
1421477_at	Cplx2	complexin 2	1,30	0,0163
1430749_at	2810040C05Rik	RIKEN cDNA 2810040C05 gene	1,30	0,0417
1447504_at	NA	NA	1,30	0,0158
1455796_x_at	Olfm1	olfactomedin 1	1,29	0,0124
1453191_at	Col27a1	collagen, type XXVII, alpha 1	1,29	0,0276
1456822_at	Rad23b	RAD23b homolog (S. cerevisiae)	1,29	0,0284
1427892_at	Myo1g	myosin IG	1,29	0,0443
1428262_s_at	Hnrnpa3	heterogeneous nuclear ribonucleoprotein A3	1,29	0,0422
1442142_at	2700050L05Rik	RIKEN cDNA 2700050L05 gene	1,29	0,0122
1445718_at	NA	NA	1,29	0,0173
1417252_at	Nt5c	5',3'-nucleotidase, cytosolic	1,29	0,0342
1421534_at	LOC14210	hypothetical LOC14210	1,29	0,0443
1433976_at	Reep3	receptor accessory protein 3	1,29	0,0209
1425410_at	Tprkb	Tp53rk binding protein	1,29	0,0075
1447284_at	Trem1	triggering receptor expressed on myeloid cells 1	1,29	0,0312
1458115_at	4930512H18Rik	RIKEN cDNA 4930512H18 gene	1,29	0,0210
1426382_at	Ppm1b	protein phosphatase 1B, magnesium dependent, beta isoform	1,29	0,0028
1458781_at	NA	NA	1,29	0,0192
1456656_at	Lin7a	lin-7 homolog A (C. elegans)	1,29	0,0352
1453426_a_at	Wdfy1	WD repeat and FYVE domain containing 1	1,29	0,0252
1418733_at	Twist1	twist homolog 1 (Drosophila)	1,29	0,0330
1436807_x_at	Trim62	tripartite motif-containing 62	1,29	0,0368
1456315_a_at	Ptpla	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a	1,29	0,0111
1419207_at	Zfp37	zinc finger protein 37	1,29	0,0241
1419217_at	Sergef	secretion regulating guanine nucleotide exchange factor	1,29	0,0141
1459248_at	NA	NA	1,29	0,0464
1420295_x_at	Clcn5	chloride channel 5	1,29	0,0062
1455333_at	Tns3	tensin 3	1,28	0,0220
1458850_at	NA	NA	1,28	0,0381

1436984_at	Abi2	abl-interactor 2	1,28	0,0452
1442065_at	Arhgap17	Rho GTPase activating protein 17	1,28	0,0213
1450026_a_at	B3gnt2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	1,28	0,0137
1437080_s_at	OTTMUSG00000015538	predicted gene, OTTMUSG00000015538	1,28	0,0308
1445687_at	Gm885	gene model 885, (NCBI)	1,28	0,0409
1442352_at	9430091N11Rik	RIKEN cDNA 9430091N11 gene	1,28	0,0242
1452243_at	Kcnj14	potassium inwardly-rectifying channel, subfamily J, member 14	1,28	0,0477
1459657_s_at	OTTMUSG00000008305	predicted gene, OTTMUSG00000008305	1,28	0,0254
1416257_at	Capn2	calpain 2	1,28	0,0234
1454979_at	Diap1	diaphanous homolog 1 (Drosophila)	1,28	0,0026
1433786_x_at	Serf2	small EDRK-rich factor 2	1,28	0,0326
1417349_at	Pldn	pallidin	1,28	0,0248
1454369_a_at	Nfatc4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	1,28	0,0054
1419694_at	St8sia1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	1,28	0,0393
1427142_s_at	Jarid1b	jumonji, AT rich interactive domain 1B (Rbp2 like)	1,28	0,0449
1429345_at	Tubgcp4	tubulin, gamma complex associated protein 4	1,28	0,0181
1439758_at	Als2cr12	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 12 (human)	1,28	0,0202
1437197_at	Sorbs2	sorbin and SH3 domain containing 2	1,28	0,0385
1423783_at	Tor2a	torsin family 2, member A	1,28	0,0483
1416605_at	Nhp2	NHP2 ribonucleoprotein homolog (yeast)	1,28	0,0435
1439888_at	NA	NA	1,28	0,0130
1417675_a_at	Mdn1	midasin homolog (yeast)	1,28	0,0335
1449976_a_at	Gpr35	G protein-coupled receptor 35	1,28	0,0144
1437855_at	Mtap4	microtubule-associated protein 4	1,28	0,0205
1460231_at	Irf5	interferon regulatory factor 5	1,28	0,0211
1417763_at	Ssr1	signal sequence receptor, alpha	1,27	0,0241
1416260_a_at	Snx1	sorting nexin 1	1,27	0,0264
1432643_at	4933411E06Rik	RIKEN cDNA 4933411E06 gene	1,27	0,0354
1438958_x_at	Fkbp1a	FK506 binding protein 1a	1,27	0,0223
1422602_a_at	Wnt5b	wingless-related MMTV integration site 5B	1,27	0,0362
1424327_at	3200002M19Rik	RIKEN cDNA 3200002M19 gene	1,27	0,0091
1447320_x_at	OTTMUSG00000008305	predicted gene, OTTMUSG00000008305	1,27	0,0106
1430311_at	Marcks	myristoylated alanine rich protein kinase C substrate	1,27	0,0425
1443267_at	NA	NA	1,27	0,0312
1424780_a_at	Reep3	receptor accessory protein 3	1,27	0,0168
1450455_s_at	Akr1c12	aldo-keto reductase family 1, member C12	1,27	0,0205
1417559_at	Sfxn1	sideroflexin 1	1,27	0,0356
1426565_at	Igf1r	insulin-like growth factor I receptor	1,27	0,0437
1427670_a_at	Tcf12	transcription factor 12	1,27	0,0232
1424572_a_at	H2afy	H2A histone family, member Y	1,27	0,0285
1442914_at	NA	NA	1,27	0,0288
1445093_at	NA	NA	1,27	0,0415
1450107_a_at	Renbp	renin binding protein	1,27	0,0468
1437393_at	Prkca	protein kinase C, alpha	1,27	0,0442
1443911_at	NA	NA	1,27	0,0131
1417790_at	Dok1	docking protein 1	1,27	0,0254

1452237_at	Agfg1	ArfGAP with FG repeats 1	1,27	0,0200
1418954_at	Camkk1	calcium/calmodulin-dependent protein kinase kinase 1, alpha	1,27	0,0074
1448832_a_at	Cplx1	complexin 1	1,27	0,0354
1419034_at	Csnk2a1	casein kinase 2, alpha 1 polypeptide	1,27	0,0152
1417032_at	Ube2g2	ubiquitin-conjugating enzyme E2G 2	1,27	0,0155
1416280_at	Uba2	ubiquitin-like modifier activating enzyme 2	1,27	0,0097
1452631_at	Rufy2	RUN and FYVE domain-containing 2	1,27	0,0249
1436237_at	Ttc9	tetratricopeptide repeat domain 9	1,27	0,0148
1418672_at	Akr1c13	aldo-keto reductase family 1, member C13	1,27	0,0475
1432926_at	NA	NA	1,26	0,0488
1419493_a_at	Tpd52	tumor protein D52	1,26	0,0023
1439911_at	NA	NA	1,26	0,0492
1456195_x_at	Itgb5	integrin beta 5	1,26	0,0242
1435345_at	Cercam	cerebral endothelial cell adhesion molecule	1,26	0,0149
1417853_at	Clca1	chloride channel calcium activated 1	1,26	0,0267
1428018_a_at	AF251705	cDNA sequence AF251705	1,26	0,0101
1440295_at	1110057K04Rik	RIKEN cDNA 1110057K04 gene	1,26	0,0449
1448328_at	Sh3bp2	SH3-domain binding protein 2	1,26	0,0340
1455162_at	Ttc39a	tetratricopeptide repeat domain 39A	1,26	0,0314
1447006_at	NA	NA	1,26	0,0079
1453175_at	Zbtb25	zinc finger and BTB domain containing 25	1,26	0,0394
1458588_at	NA	NA	1,26	0,0237
1439106_at	Zfp462	zinc finger protein 462	1,26	0,0417
1446026_at	NA	NA	1,26	0,0441
1455962_at	Hhat	hedgehog acyltransferase	1,26	0,0341
1415870_at	Calu	calumenin	1,26	0,0299
1458849_at	Asah2	N-acylsphingosine amidohydrolase 2	1,26	0,0158
1437280_s_at	Serbp1	serpine1 mRNA binding protein 1	1,26	0,0048
1435519_at	LOC100048397	similar to GTP-binding protein (smg p21B)	1,26	0,0407
1456476_at	Atxn2l	ataxin 2-like	1,26	0,0308
1452362_at	Trim16	tripartite motif-containing 16	1,26	0,0138
1426165_a_at	Casp3	caspase 3	1,26	0,0470
1445079_at	NA	NA	1,26	0,0467
1457416_at	NA	NA	1,26	0,0111
1433674_a_at	Snord22	small nucleolar RNA, C/D box 22	1,26	0,0232
1445101_at	NA	NA	1,26	0,0345
1431003_a_at	2610002J02Rik	RIKEN cDNA 2610002J02 gene	1,26	0,0413
1440209_at	Mrz 01	membrane-associated ring finger (C3HC4) 1	1,26	0,0166
1421943_at	Tgfa	transforming growth factor alpha	1,26	0,0389
1418067_at	Cfl2	cofilin 2, muscle	1,25	0,0098
1457804_at	NA	NA	1,25	0,0323
1420570_x_at	Tcl1b3	T-cell leukemia/lymphoma 1B, 3	1,25	0,0197
1442248_at	NA	NA	1,25	0,0324
1438726_at	Mical2	microtubule associated monoxygenase, calponin and LIM domain containing 2	1,25	0,0234
1453276_at	Kif13b	kinesin family member 13B	1,25	0,0411
1416234_at	Lrrc59	leucine rich repeat containing 59	1,25	0,0373
1456694_x_at	Ptpn6	protein tyrosine phosphatase, non-receptor type 6	1,25	0,0213
1448467_a_at	Ehbp1l1	EH domain binding protein 1-like 1	1,25	0,0087
1448903_at	Sep 15	selenoprotein	1,25	0,0080
1446512_at	Zc3h15	zinc finger CCCH-type containing 15	1,25	0,0420
1454447_at	5830434F19	RIKEN cDNA 5830434F19 gene	1,25	0,0178

	Rik			
1448137_at	Aldh7a1	aldehyde dehydrogenase family 7, member A1	1,25	0,0388
1437683_x_at	Serf2	small EDRK-rich factor 2	1,25	0,0420
1422507_at	Cstb	cystatin B	1,25	0,0073
1459522_s_at	Gyg	glycogenin	1,25	0,0066
1447285_at	NA	NA	1,25	0,0173
1441792_at	A630033E08Rik	RIKEN cDNA A630033E08 gene	1,25	0,0048
1423174_a_at	Pard6b	par-6 (partitioning defective 6) homolog beta (C. elegans)	1,25	0,0331
1433120_at	9530002O20Rik	RIKEN cDNA 9530002O20 gene	1,25	0,0437
1444696_at	BC059841	cDNA sequence BC059841	1,25	0,0411
1459918_at	Bub3	budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae)	1,25	0,0447
1448622_at	Lsm4	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	1,25	0,0117
1423369_at	Fmr1	fragile X mental retardation syndrome 1 homolog	1,25	0,0437
1434797_at	6720469N11Rik	RIKEN cDNA 6720469N11 gene	1,25	0,0151
1449293_a_at	Skp2	S-phase kinase-associated protein 2 (p45)	1,25	0,0335
1418073_at	Acot9	acyl-CoA thioesterase 9	1,24	0,0079
1419115_at	Alg14	asparagine-linked glycosylation 14 homolog (yeast)	1,24	0,0146
1431843_a_at	Nfkbie	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	1,24	0,0214
1457769_at	H60a	histocompatibility 60a	1,24	0,0111
1426570_a_at	Frk	fyn-related kinase	1,24	0,0415
1448933_at	Pcdhb17	protocadherin beta 17	1,24	0,0413
1437903_at	Lox	lysyl oxidase	1,24	0,0414
1451037_at	Ptpn9	protein tyrosine phosphatase, non-receptor type 9	1,24	0,0333
1424047_at	Dera	2-deoxyribose-5-phosphate aldolase homolog (C. elegans)	1,24	0,0242
1456111_at	Fam55d	family with sequence similarity 55, member D	1,24	0,0251
1423182_at	Tnfrsf13b	tumor necrosis factor receptor superfamily, member 13b	1,24	0,0119
1447495_at	Fank1	fibronectin type 3 and ankyrin repeat domains 1	1,24	0,0446
1454416_at	5730575I04Rik	RIKEN cDNA 5730575I04 gene	1,24	0,0370
1457578_at	NA	NA	1,24	0,0497
1434639_at	Klhl29	kelch-like 29 (Drosophila)	1,24	0,0219
1416582_a_at	Bad	BCL2-associated agonist of cell death	1,24	0,0366
1416563_at	Ctps	cytidine 5'-triphosphate synthase	1,24	0,0313
1420197_at	Gadd45b	growth arrest and DNA-damage-inducible 45 beta	1,24	0,0405
1422707_at	Pik3cg	phosphoinositide-3-kinase, catalytic, gamma polypeptide	1,24	0,0164
1457827_at	Arsj	arylsulfatase J	1,24	0,0145
1447274_at	NA	NA	1,24	0,0225
1427878_at	0610010O12Rik	RIKEN cDNA 0610010O12 gene	1,24	0,0288
1457308_at	NA	NA	1,24	0,0286
1437466_at	Alcam	activated leukocyte cell adhesion molecule	1,24	0,0272
1438137_at	NA	NA	1,24	0,0365
1422922_at	Recql4	RecQ protein-like 4	1,24	0,0226
1449368_at	Dcn	decorin	1,23	0,0173
1459298_at	Aebp1	AE binding protein 1	1,23	0,0454
1442175_at	C030027H14Rik	RIKEN cDNA C030027H14 gene	1,23	0,0358
1435665_at	AI451617	expressed sequence AI451617	1,23	0,0100

1420502_at	Sat1	spermidine/spermine N1-acetyl transferase 1	1,23	0,0376
1423654_a_at	Rnf4	ring finger protein 4	1,23	0,0385
1438629_x_at	Grn	granulin	1,23	0,0393
1432331_a_at	Prrx2	paired related homeobox 2	1,23	0,0449
1418097_a_at	Crlf2	cytokine receptor-like factor 2	1,23	0,0400
1449821_a_at	Memo1	mediator of cell motility 1	1,23	0,0047
1422259_a_at	Ccr5	chemokine (C-C motif) receptor 5	1,23	0,0493
1428488_at	Pigk	phosphatidylinositol glycan anchor biosynthesis, class K	1,23	0,0244
1455921_at	Ttc30a2	tetratricopeptide repeat domain 30A2	1,23	0,0397
1460118_at	NA	NA	1,23	0,0385
1426825_at	Fmnl3	formin-like 3	1,23	0,0073
1436117_at	A830010M20Rik	RIKEN cDNA A830010M20 gene	1,23	0,0156
1439545_at	NA	NA	1,23	0,0415
1420563_at	Gria3	glutamate receptor, ionotropic, AMPA3 (alpha 3)	1,23	0,0470
1429783_at	Pdlim5	PDZ and LIM domain 5	1,23	0,0051
1456344_at	Tnc	tenascin C	1,23	0,0352
1417825_at	Esd	esterase D/formylglutathione hydrolase	1,23	0,0055
1450697_at	Slc30a7	solute carrier family 30 (zinc transporter), member 7	1,23	0,0303
1438753_at	NA	NA	1,22	0,0381
1434991_at	Fbxw17	F-box and WD-40 domain protein 17	1,22	0,0302
1436945_x_at	LOC100045432	similar to Stromal interaction molecule 1	1,22	0,0381
1418638_at	H2-DMb1	histocompatibility 2, class II, locus Mb1	1,22	0,0179
1422553_at	Pten	phosphatase and tensin homolog	1,22	0,0166
1436928_s_at	Cenpo	centromere protein O	1,22	0,0087
1441657_at	NA	NA	1,22	0,0338
1417652_a_at	Tbca	tubulin cofactor A	1,22	0,0126
1454343_at	6430710M23Rik	RIKEN cDNA 6430710M23 gene	1,22	0,0274
1421564_at	Serpina3c	serine (or cysteine) peptidase inhibitor, clade A, member 3C	1,22	0,0374
1437155_a_at	Wwtr1	WW domain containing transcription regulator 1	1,22	0,0190
1458507_at	Rnf216	ring finger protein 216	1,22	0,0449
1421707_at	Tmc2	transmembrane channel-like gene family 2	1,22	0,0467
1425248_a_at	Tyro3	TYRO3 protein tyrosine kinase 3	1,22	0,0112
1447797_x_at	Pih1d1	PIH1 domain containing 1	1,22	0,0475
1454639_x_at	Rpl41	ribosomal protein L41	1,22	0,0086
1447813_x_at	Sla	src-like adaptor	1,22	0,0256
1443199_at	Lrch3	leucine-rich repeats and calponin homology (CH) domain containing 3	1,22	0,0482
1442540_at	C77609	expressed sequence C77609	1,22	0,0471
1460292_a_at	Smarca1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	1,22	0,0220
1449750_at	AA407331	expressed sequence AA407331	1,22	0,0484
1446791_at	NA	NA	1,22	0,0488
1424304_at	Tpcn2	two pore segment channel 2	1,22	0,0481
1435878_at	Stk38l	serine/threonine kinase 38 like	1,22	0,0147
1441555_at	NA	NA	1,22	0,0379
1443542_at	NA	NA	1,22	0,0497
1450595_at	V1rc1	vomeronasal 1 receptor, C1	1,21	0,0461
1416087_at	Ap1s1	adaptor protein complex AP-1, sigma 1	1,21	0,0365
1456652_at	Dtl	denticleless homolog (Drosophila)	1,21	0,0465
1416995_at	Pacsin3	protein kinase C and casein kinase substrate in neurons 3	1,21	0,0445
1444547_at	NA	NA	1,21	0,0318

1420361_at	Slc11a1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	1,21	0,0247
1423732_at	Tram1	translocating chain-associating membrane protein 1	1,21	0,0466
1443136_at	LOC432459	hypothetical gene supported by AK082906	1,21	0,0369
1443141_at	NA	NA	1,21	0,0413
1432794_at	2310058F05Rik	RIKEN cDNA 2310058F05 gene	1,21	0,0175
1433846_s_at	Fam175b	family with sequence similarity 175, member B	1,21	0,0350
1447120_at	NA	NA	1,21	0,0293
1446356_at	NA	NA	1,21	0,0263
1421930_at	Icos	inducible T-cell co-stimulator	1,21	0,0274
1415804_at	Cx3cl1	chemokine (C-X3-C motif) ligand 1	1,21	0,0341
1458276_x_at	Cit	citron	1,21	0,0413
1418406_at	Pde8a	phosphodiesterase 8A	1,21	0,0270
1423113_a_at	Ube2d3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	1,21	0,0433
1437274_at	Copa	coatomer protein complex subunit alpha	1,21	0,0304
1427023_at	Phyhipl	phytanoyl-CoA hydroxylase interacting protein-like	1,21	0,0402
1448679_at	Hyal2	hyaluronoglucosaminidase 2	1,21	0,0363
1441675_at	NA	NA	1,21	0,0386
1423955_a_at	Lass2	LAG1 homolog, ceramide synthase 2	1,20	0,0354
1455955_s_at	Snx17	sorting nexin 17	1,20	0,0470
1434005_at	Rbms1	RNA binding motif, single stranded interacting protein 1	1,20	0,0462
1436260_at	NA	NA	1,20	0,0270
1448714_at	Rngtt	RNA guanylyltransferase and 5'-phosphatase	1,20	0,0205
1457209_at	Ddhd2	DDHD domain containing 2	1,20	0,0418
1438833_at	Casc5	cancer susceptibility candidate 5	1,20	0,0405
1451466_at	D16Ertd472e	DNA segment, Chr 16, ERATO Doi 472, expressed	1,20	0,0461
1446613_at	NA	NA	1,20	0,0267
1456567_x_at	Grn	granulin	1,20	0,0323
1416526_a_at	Park7	Parkinson disease (autosomal recessive, early onset) 7	1,20	0,0353
1453833_a_at	Rnaseh1	ribonuclease H1	1,20	0,0204
1452091_a_at	Rbm28	RNA binding motif protein 28	1,20	0,0441
1450481_at	Mybl1	myeloblastosis oncogene-like 1	1,20	0,0380
1444138_at	Cyp2r1	cytochrome P450, family 2, subfamily r, polypeptide 1	1,20	0,0493
1422932_a_at	Vav1	vav 1 oncogene	1,20	0,0244
1443524_x_at	Bcl10	B-cell leukemia/lymphoma 10	1,20	0,0461
1452196_a_at	Nckap1	NCK-associated protein 1	1,20	0,0189
1459886_at	NA	NA	1,20	0,0470
1435739_at	Lats1	large tumor suppressor	1,20	0,0479
1428738_a_at	D14Ertd449e	DNA segment, Chr 14, ERATO Doi 449, expressed	1,20	0,0498
1423296_at	Psmd8	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	1,19	0,0117
1426299_at	Snx20	sorting nexin 20	1,19	0,0494
1417204_at	Kdelr2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	1,19	0,0437
1458416_at	A330048O09Rik	RIKEN cDNA A330048O09 gene	1,19	0,0283
1422881_s_at	Sypl	synaptophysin-like protein	1,19	0,0283
1431597_a_at	Nrip3	nuclear receptor interacting protein 3	1,19	0,0379
1427445_a_at	Ttn	titin	1,19	0,0095
1427515_at	Pion	pigeon homolog (Drosophila)	1,19	0,0217
1441448_at	Pum2	pumilio 2 (Drosophila)	1,19	0,0181

1432189_a_at	Sox5	SRY-box containing gene 5	1,19	0,0418
1426922_s_at	Agfg1	ArfGAP with FG repeats 1	1,19	0,0417
1459236_at	AU022436	expressed sequence AU022436	1,19	0,0203
1429544_at	1700029J11Rik	RIKEN cDNA 1700029J11 gene	1,19	0,0386
1443422_at	2410089E03Rik	RIKEN cDNA 2410089E03 gene	1,19	0,0425
1452566_at	NA	NA	1,19	0,0466
1440019_at	NA	NA	1,19	0,0388
1419545_a_at	Atp6v1c1	ATPase, H+ transporting, lysosomal V1 subunit C1	1,19	0,0335
1447716_x_at	6330442E10Rik	RIKEN cDNA 6330442E10 gene	1,18	0,0384
1428094_at	Lamp2	lysosomal-associated membrane protein 2	1,18	0,0084
1451101_a_at	Rps28	ribosomal protein S28	1,18	0,0315
1425841_at	Slc26a7	solute carrier family 26, member 7	1,18	0,0306
1459418_at	NA	NA	1,18	0,0306
1438893_at	5530601H04Rik	RIKEN cDNA 5530601H04 gene	1,18	0,0240
1435615_at	Zfp365	zinc finger protein 365	1,18	0,0361
1423917_a_at	Cttn	cortactin	1,18	0,0241
1436867_at	Srl	sarcalumenin	1,18	0,0383
1451973_at	Uba5	ubiquitin-like modifier activating enzyme 5	1,17	0,0234
1415962_at	Eif3h	eukaryotic translation initiation factor 3, subunit H	1,17	0,0398
1431699_at	Fut4-ps1	fucosyltransferase 4, pseudogene 1	1,17	0,0353
1456674_at	E130016E03Rik	RIKEN cDNA E130016E03 gene	1,17	0,0449
1435029_at	NA	NA	1,17	0,0470
1455964_at	Crkrs	CDC2-related kinase, arginine/serine-rich	1,17	0,0490
1416025_at	Fgg	fibrinogen, gamma polypeptide	1,17	0,0381
1432807_at	5830426K05Rik	RIKEN cDNA 5830426K05 gene	1,17	0,0339
1445647_at	AI447881	expressed sequence AI447881	1,17	0,0377
1420471_at	Hcrt	hypocretin	1,16	0,0379
1440082_at	Ptk2	PTK2 protein tyrosine kinase 2	1,16	0,0214
1456807_at	Ppp1r3e	protein phosphatase 1, regulatory (inhibitor) subunit 3E	1,16	0,0417
1434595_at	Trim9	tripartite motif-containing 9	1,16	0,0270
1424741_s_at	Creb3	cAMP responsive element binding protein 3	1,16	0,0411
1420820_at	2900073G15Rik	RIKEN cDNA 2900073G15 gene	1,15	0,0417
1440906_at	NA	NA	1,14	0,0309
1422846_at	Rbp2	retinol binding protein 2, cellular	1,14	0,0370
1447123_at	NA	NA	1,13	0,0437

Downregulated in TAC vs. Sham

Affymetrix probe set identification	Gene symbol	Gene name	Fold change	Adjusted *P* value
1434672_at	Gpr22	G protein-coupled receptor 22	0,17	0,0001
1434673_at	Gpr22	G protein-coupled receptor 22	0,21	0,0009
1445764_at	NA	NA	0,24	0,0011
1426672_at	Ano10	anoctamin 10	0,28	0,0008
1418219_at	Il15	interleukin 15	0,28	0,0000
1444153_at	NA	NA	0,29	0,0003
1444025_at	Kcnj3	potassium inwardly-rectifying channel, subfamily J, member 3	0,30	0,0003
1454850_at	Tbc1d10c	TBC1 domain family, member 10c	0,30	0,0087
1439801_at	Sunc1	Sad1 and UNC84 domain containing 1	0,31	0,0177
1423183_at	Lgi1	leucine-rich repeat LGI family, member 1	0,31	0,0011
1435370_a_at	Ces3	carboxylesterase 3	0,32	0,0006
1447830_s_at	Rgs2	regulator of G-protein signaling 2	0,33	0,0000
1449081_at	Ces3	carboxylesterase 3	0,34	0,0002
1423085_at	Efnb3	ephrin B3	0,34	0,0000
1427213_at	Pfkfb1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	0,35	0,0001
1418174_at	Dbp	D site albumin promoter binding protein	0,35	0,0415
1425645_s_at	Cyp2b10	cytochrome P450, family 2, subfamily b, polypeptide 10	0,37	0,0026
1436833_x_at	Ttll1	tubulin tyrosine ligase-like 1	0,37	0,0424
1422651_at	Adipoq	adiponectin, C1Q and collagen domain containing	0,37	0,0277
1455374_at	Kcnj3	potassium inwardly-rectifying channel, subfamily J, member 3	0,38	0,0000
1452888_at	1110034G24Rik	RIKEN cDNA 1110034G24 gene	0,39	0,0069
1423436_at	Gsta3	glutathione S-transferase, alpha 3	0,39	0,0403
1434647_at	Egflam	EGF-like, fibronectin type III and laminin G domains	0,39	0,0001
1452476_at	Cacnb2	calcium channel, voltage-dependent, beta 2 subunit	0,40	0,0109
1438211_s_at	Dbp	D site albumin promoter binding protein	0,40	0,0304
1425164_a_at	Phkg1	phosphorylase kinase gamma 1	0,40	0,0006
1418697_at	Inmt	indolethylamine N-methyltransferase	0,40	0,0177
1449407_at	Ift81	intraflagellar transport 81 homolog (Chlamydomonas)	0,40	0,0001
1419551_s_at	Stk39	serine/threonine kinase 39, STE20/SPS1 homolog (yeast)	0,40	0,0002
1437617_x_at	1110034G24Rik	RIKEN cDNA 1110034G24 gene	0,41	0,0025
1458081_at	NA	NA	0,41	0,0402
1422257_s_at	Cyp2b10	cytochrome P450, family 2, subfamily b, polypeptide 10	0,41	0,0059
1452086_at	Trmt5	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae)	0,41	0,0000
1438217_at	A2bp1	ataxin 2 binding protein 1	0,41	0,0017
1429021_at	Epha4	Eph receptor A4	0,42	0,0001
1417382_at	Entpd5	ectonucleoside triphosphate diphosphohydrolase 5	0,42	0,0003
1451204_at	Scara5	scavenger receptor class A, member 5 (putative)	0,42	0,0004
1428892_at	Ppil1	peptidylprolyl isomerase (cyclophilin)-like 1	0,42	0,0001
1417814_at	Pla2g5	phospholipase A2, group V	0,43	0,0006
1455358_at	A2bp1	ataxin 2 binding protein 1	0,43	0,0100
1449015_at	Retnla	resistin like alpha	0,43	0,0134
1421928_at	Epha4	Eph receptor A4	0,43	0,0037
1434735_at	Hlf	hepatic leukemia factor	0,44	0,0026
1422677_at	Dgat2	diacylglycerol O-acyltransferase 2	0,44	0,0209

1458040_at	NA	NA	0,44	0,0169
1419286_s_at	Ift81	intraflagellar transport 81 homolog (Chlamydomonas)	0,44	0,0001
1456401_at	Cacnb2	calcium channel, voltage-dependent, beta 2 subunit	0,44	0,0008
1434736_at	Hlf	hepatic leukemia factor	0,44	0,0034
1448130_at	Fdft1	farnesyl diphosphate farnesyl transferase 1	0,45	0,0001
1435371_x_at	Ces3	carboxylesterase 3	0,45	0,0068
1439066_at	Angpt1	angiopoietin 1	0,45	0,0399
1428812_at	1700040L02Rik	RIKEN cDNA 1700040L02 gene	0,45	0,0421
1443551_at	Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	0,45	0,0152
1417383_at	Entpd5	ectonucleoside triphosphate diphosphohydrolase 5	0,45	0,0006
1418314_a_at	A2bp1	ataxin 2 binding protein 1	0,45	0,0031
1441937_s_at	LOC100047214	similar to PTEN induced putative kinase 1	0,46	0,0202
1427038_at	Penk1	preproenkephalin 1	0,46	0,0188
1441867_x_at	4930534B04Rik	RIKEN cDNA 4930534B04 gene	0,46	0,0140
1417765_a_at	Amy1	amylase 1, salivary	0,46	0,0076
1422315_x_at	Phkg1	phosphorylase kinase gamma 1	0,46	0,0014
1419550_a_at	Stk39	serine/threonine kinase 39, STE20/SPS1 homolog (yeast)	0,46	0,0082
1420638_at	Prps2	phosphoribosyl pyrophosphate synthetase 2	0,46	0,0155
1437953_at	Prei4	preimplantation protein 4	0,46	0,0132
1439143_at	A930018M24Rik	RIKEN cDNA A930018M24 gene	0,47	0,0161
1419340_at	Mov10l1	Moloney leukemia virus 10-like 1	0,47	0,0009
1453355_at	Wnk2	WNK lysine deficient protein kinase 2	0,47	0,0001
1421468_at	Kcnj3	potassium inwardly-rectifying channel, subfamily J, member 3	0,47	0,0008
1417384_at	Entpd5	ectonucleoside triphosphate diphosphohydrolase 5	0,47	0,0011
1450699_at	Selenbp1	selenium binding protein 1	0,48	0,0346
1417168_a_at	Usp2	ubiquitin specific peptidase 2	0,48	0,0023
1456824_at	Zfp612	zinc finger protein 612	0,48	0,0016
1448956_at	Stard10	START domain containing 10	0,48	0,0015
1419248_at	Rgs2	regulator of G-protein signaling 2	0,48	0,0062
1424531_a_at	Tcea3	transcription elongation factor A (SII), 3	0,48	0,0001
1429228_at	4930534B04Rik	RIKEN cDNA 4930534B04 gene	0,48	0,0220
1447462_at	D7Wsu130e	DNA segment, Chr 7, Wayne State University 130, expressed	0,48	0,0060
1435751_at	Abcc9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	0,48	0,0008
1451606_at	A530016L24Rik	RIKEN cDNA A530016L24 gene	0,48	0,0150
1416225_at	Adh1	alcohol dehydrogenase 1 (class I)	0,48	0,0158
1457066_at	Abcc8	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	0,49	0,0276
1441590_at	Kcnj5	potassium inwardly-rectifying channel, subfamily J, member 5	0,49	0,0324
1423577_at	Ankrd32	ankyrin repeat domain 32	0,49	0,0000
1455475_at	3110057O12Rik	RIKEN cDNA 3110057O12 gene	0,49	0,0070
1427736_a_at	Ccrl2	chemokine (C-C motif) receptor-like 2	0,49	0,0111
1420408_a_at	Abcc9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	0,49	0,0009
1422678_at	Dgat2	diacylglycerol O-acyltransferase 2	0,49	0,0002
1448607_at	Nampt	nicotinamide phosphoribosyltransferase	0,49	0,0289

1434354_at	Maob	monoamine oxidase B	0,49	0,0003
1435991_at	Nr3c2	nuclear receptor subfamily 3, group C, member 2	0,49	0,0018
1418186_at	Gstt1	glutathione S-transferase, theta 1	0,50	0,0003
1438322_x_at	Fdft1	farnesyl diphosphate farnesyl transferase 1	0,50	0,0014
1458324_x_at	NA	NA	0,50	0,0027
1417702_a_at	Hnmt	histamine N-methyltransferase	0,50	0,0237
1436619_at	D630045M09Rik	RIKEN cDNA D630045M09 gene	0,50	0,0048
1434100_x_at	NA	NA	0,50	0,0316
1421087_at	Per3	period homolog 3 (Drosophila)	0,50	0,0477
1448825_at	Pdk2	pyruvate dehydrogenase kinase, isoenzyme 2	0,50	0,0004
1436041_at	LOC100046086	similar to dHand protein	0,50	0,0052
1435658_at	Slc27a1	solute carrier family 27 (fatty acid transporter), member 1	0,50	0,0006
1428513_at	Calcoco1	calcium binding and coiled coil domain 1	0,50	0,0013
1438734_at	A530016L24Rik	RIKEN cDNA A530016L24 gene	0,50	0,0332
1451229_at	Hdac11	histone deacetylase 11	0,50	0,0049
1435188_at	Gm129	gene model 129, (NCBI)	0,50	0,0436
1421456_at	P2ry1	purinergic receptor P2Y, G-protein coupled 1	0,51	0,0412
1435254_at	Plxnb1	plexin B1	0,51	0,0004
1417580_s_at	Selenbp2	selenium binding protein 2	0,51	0,0447
1439352_at	Trim7	tripartite motif-containing 7	0,51	0,0001
1420444_at	Slc22a3	solute carrier family 22 (organic cation transporter), member 3	0,51	0,0031
1427104_at	Zfp612	zinc finger protein 612	0,51	0,0001
1452973_at	Ppm1k	protein phosphatase 1K (PP2C domain containing)	0,51	0,0002
1430787_at	2310050B05Rik	RIKEN cDNA 2310050B05 gene	0,51	0,0420
1434099_at	NA	NA	0,51	0,0375
1460518_at	E130119H09Rik	RIKEN cDNA E130119H09 gene	0,51	0,0073
1416950_at	Tnfaip8	tumor necrosis factor, alpha-induced protein 8	0,51	0,0159
1422183_a_at	Adra1b	adrenergic receptor, alpha 1b	0,51	0,0116
1460081_at	Syt7	synaptotagmin VII	0,51	0,0008
1455372_at	Cpeb3	cytoplasmic polyadenylation element binding protein 3	0,51	0,0080
1435694_at	Arhgap26	Rho GTPase activating protein 26	0,51	0,0024
1419247_at	Rgs2	regulator of G-protein signaling 2	0,52	0,0213
1419072_at	Gstm7	glutathione S-transferase, mu 7	0,52	0,0005
1424737_at	Thrsp	thyroid hormone responsive SPOT14 homolog (Rattus)	0,52	0,0013
1435285_at	Mpped2	metallophosphoesterase domain containing 2	0,52	0,0018
1448502_at	Slc16a7	solute carrier family 16 (monocarboxylic acid transporters), member 7	0,52	0,0288
1451765_a_at	Entpd5	ectonucleoside triphosphate diphosphohydrolase 5	0,52	0,0003
1437424_at	Syde2	synapse defective 1, Rho GTPase, homolog 2 (C. elegans)	0,52	0,0037
1435626_a_at	Herpud1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	0,52	0,0068
1456911_at	Clasp2	CLIP associating protein 2	0,52	0,0290
1422811_at	Slc27a1	solute carrier family 27 (fatty acid transporter), member 1	0,52	0,0037
1439301_at	NA	NA	0,52	0,0122
1424669_at	Zfyve21	zinc finger, FYVE domain containing 21	0,52	0,0007
1431074_a_at	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	0,52	0,0034
1440435_at	Ky	kyphoscoliosis peptidase	0,52	0,0025
1447693_s_at	Neo1	neogenin	0,52	0,0009
1448949_at	Car4	carbonic anhydrase 4	0,52	0,0083
1452940_x_at	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	0,52	0,0045

1424226_at	9030617O03Rik	RIKEN cDNA 9030617O03 gene	0,53	0,0012
1437765_at	Cpeb3	cytoplasmic polyadenylation element binding protein 3	0,53	0,0101
1437243_at	D2hgdh	D-2-hydroxyglutarate dehydrogenase	0,53	0,0161
1440537_at	Kcnv2	potassium channel, subfamily V, member 2	0,53	0,0010
1431220_at	2810416G20Rik	RIKEN cDNA 2810416G20 gene	0,53	0,0028
1441940_x_at	Klhdc8a	kelch domain containing 8A	0,53	0,0255
1423086_at	Npc1	Niemann Pick type C1	0,53	0,0065
1454693_at	Hdac4	histone deacetylase 4	0,53	0,0010
1460281_at	Asb15	ankyrin repeat and SOCS box-containing 15	0,53	0,0303
1436521_at	Slc36a2	solute carrier family 36 (proton/amino acid symporter), member 2	0,53	0,0102
1426584_a_at	Sord	sorbitol dehydrogenase	0,53	0,0001
1444504_at	Dhrs7c	dehydrogenase/reductase (SDR family) member 7C	0,53	0,0001
1460061_at	NA	NA	0,53	0,0312
1420543_at	Dnajc28	DnaJ (Hsp40) homolog, subfamily C, member 28	0,53	0,0171
1437797_at	Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	0,53	0,0385
1431751_a_at	Mpped2	metallophosphoesterase domain containing 2	0,53	0,0037
1445708_x_at	3110021A11Rik	RIKEN cDNA 3110021A11 gene	0,53	0,0210
1450773_at	Kcnd2	potassium voltage-gated channel, Shal-related family, member 2	0,53	0,0300
1423437_at	Gsta3	glutathione S-transferase, alpha 3	0,53	0,0066
1440587_at	NA	NA	0,54	0,0043
1450468_at	Myoc	myocilin	0,54	0,0098
1421590_at	Mrgprh	MAS-related GPR, member H	0,54	0,0047
1455455_at	Glt28d2	glycosyltransferase 28 domain containing 2	0,54	0,0155
1451194_at	Aldob	aldolase B, fructose-bisphosphate	0,54	0,0054
1455541_a_at	4430402I18Rik	RIKEN cDNA 4430402I18 gene	0,54	0,0184
1450725_s_at	Car14	carbonic anhydrase 14	0,54	0,0066
1435695_a_at	Ggct	gamma-glutamyl cyclotransferase	0,54	0,0003
1452823_at	Gstk1	glutathione S-transferase kappa 1	0,54	0,0001
1460125_at	NA	NA	0,54	0,0101
1436277_at	Rnf207	ring finger protein 207	0,54	0,0003
1428878_a_at	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	0,54	0,0037
1424393_s_at	Adhfe1	alcohol dehydrogenase, iron containing, 1	0,54	0,0009
1421848_at	Slc22a5	solute carrier family 22 (organic cation transporter), member 5	0,54	0,0268
1422835_at	Kcnd2	potassium voltage-gated channel, Shal-related family, member 2	0,55	0,0069
1435171_at	2810416G20Rik	RIKEN cDNA 2810416G20 gene	0,55	0,0001
1418094_s_at	Car4	carbonic anhydrase 4	0,55	0,0131
1433763_at	Entpd5	ectonucleoside triphosphate diphosphohydrolase 5	0,55	0,0064
1449001_at	Ivd	isovaleryl coenzyme A dehydrogenase	0,55	0,0007
1435911_s_at	Slc2a12	solute carrier family 2 (facilitated glucose transporter), member 12	0,55	0,0025
1419056_at	Rtn2	reticulon 2 (Z-band associated protein)	0,55	0,0001
1417812_a_at	Lamb3	laminin, beta 3	0,55	0,0296
1437287_at	1110020G09Rik	RIKEN cDNA 1110020G09 gene	0,55	0,0051
1418715_at	Pank1	pantothenate kinase 1	0,55	0,0033
1451322_at	Cmbl	carboxymethylenebutenolidase-like (Pseudomonas)	0,55	0,0168
1424790_at	Slc25a42	solute carrier family 25, member 42	0,55	0,0145

1426876_at	Pm20d1	peptidase M20 domain containing 1	0,55	0,0118
1448185_at	Herpud1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	0,55	0,0240
1449398_at	Rpl3l	ribosomal protein L3-like	0,56	0,0005
1435097_at	Mmab	methylmalonic aciduria (cobalamin deficiency) type B homolog (human)	0,56	0,0054
1455506_at	Slc25a34	solute carrier family 25, member 34	0,56	0,0018
1448330_at	Gstm1	glutathione S-transferase, mu 1	0,56	0,0183
1426263_at	Cadm4	cell adhesion molecule 4	0,56	0,0004
1434931_at	Neo1	neogenin	0,56	0,0014
1437385_at	Ccbe1	collagen and calcium binding EGF domains 1	0,56	0,0005
1421277_at	Spna1	spectrin alpha 1	0,56	0,0021
1417823_at	Gcat	glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	0,56	0,0003
1453687_at	Slc4a3	solute carrier family 4 (anion exchanger), member 3	0,56	0,0045
1433532_a_at	Mbp	myelin basic protein	0,56	0,0338
1416647_at	Bckdha	branched chain ketoacid dehydrogenase E1, alpha polypeptide	0,56	0,0019
1449547_at	Asb14	ankyrin repeat and SOCS box-containing 14	0,56	0,0156
1418497_at	Fgf13	fibroblast growth factor 13	0,56	0,0004
1424392_at	Adhfe1	alcohol dehydrogenase, iron containing, 1	0,56	0,0062
1417649_at	Cdkn1c	cyclin-dependent kinase inhibitor 1C (P57)	0,56	0,0162
1434831_a_at	Foxo3	forkhead box O3	0,56	0,0015
1425114_at	Rbbp6	retinoblastoma binding protein 6	0,56	0,0055
1419040_at	Cyp2d22	cytochrome P450, family 2, subfamily d, polypeptide 22	0,56	0,0229
1420534_at	Gucy1a3	guanylate cyclase 1, soluble, alpha 3	0,56	0,0139
1452583_s_at	Galm	galactose mutarotase	0,57	0,0417
1449526_a_at	Gdpd3	glycerophosphodiester phosphodiesterase domain containing 3	0,57	0,0015
1443932_at	Klhdc1	kelch domain containing 1	0,57	0,0187
1422973_a_at	Thrsp	thyroid hormone responsive SPOT14 homolog (Rattus)	0,57	0,0011
1452678_a_at	Ccbl1	cysteine conjugate-beta lyase 1	0,57	0,0009
1455025_at	Paqr9	progestin and adipoQ receptor family member IX	0,57	0,0186
1454646_at	Tcp11l2	t-complex 11 (mouse) like 2	0,57	0,0076
1435529_at	OTTMUSG00000016644	predicted gene, OTTMUSG00000016644	0,57	0,0192
1449501_a_at	Gzmm	granzyme M (lymphocyte met-ase 1)	0,57	0,0013
1449443_at	Decr1	2,4-dienoyl CoA reductase 1, mitochondrial	0,57	0,0016
1458573_at	NA	NA	0,57	0,0129
1450162_at	Dpf3	D4, zinc and double PHD fingers, family 3	0,57	0,0017
1435851_at	Lgi1	leucine-rich repeat LGI family, member 1	0,57	0,0055
1420806_at	Fgf16	fibroblast growth factor 16	0,57	0,0180
1428444_at	Asb2	ankyrin repeat and SOCS box-containing 2	0,57	0,0017
1452766_at	Tppp	tubulin polymerization promoting protein	0,57	0,0030
1446582_at	Poln	DNA polymerase N	0,57	0,0103
1424715_at	Retsat	retinol saturase (all trans retinol 13,14 reductase)	0,58	0,0058
1449519_at	Gadd45a	growth arrest and DNA-damage-inducible 45 alpha	0,58	0,0056
1444429_at	Lrtm1	leucine-rich repeats and transmembrane domains 1	0,58	0,0262
1439101_at	Mylk3	myosin light chain kinase 3	0,58	0,0019
1436189_at	NA	NA	0,58	0,0009
1423892_at	Apbb1	amyloid beta (A4) precursor protein-binding, family B, member 1	0,58	0,0144
1454984_at	Lifr	leukemia inhibitory factor receptor	0,58	0,0002
1435234_at	Ncoa2	nuclear receptor coactivator 2	0,58	0,0213
1424478_at	Bbs2	Bardet-Biedl syndrome 2 (human)	0,58	0,0071
1436758_at	Hdac4	histone deacetylase 4	0,58	0,0036

1424716_at	Retsat	retinol saturase (all trans retinol 13,14 reductase)	0,58	0,0483
1434815_a_at	Mapkapk3	mitogen-activated protein kinase-activated protein kinase 3	0,58	0,0054
1427964_at	Cmtm8	CKLF-like MARVEL transmembrane domain containing 8	0,58	0,0071
1450184_s_at	Tef	thyrotroph embryonic factor	0,58	0,0200
1435461_at	Magi3	membrane associated guanylate kinase, WW and PDZ domain containing 3	0,58	0,0083
1444089_at	Spnb2	spectrin beta 2	0,58	0,0005
1426743_at	Appl2	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	0,58	0,0022
1434150_a_at	Mettl7a1	methyltransferase like 7A1	0,58	0,0013
1432472_a_at	Mccc2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	0,59	0,0478
1455214_at	Mitf	microphthalmia-associated transcription factor	0,59	0,0077
1426383_at	Cry2	cryptochrome 2 (photolyase-like)	0,59	0,0391
1448170_at	Siah2	seven in absentia 2	0,59	0,0500
1450790_at	Tg	thyroglobulin	0,59	0,0111
1424211_at	Slc25a33	solute carrier family 25, member 33	0,59	0,0342
1452173_at	Hadha	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	0,59	0,0036
1416416_x_at	Gstm1	glutathione S-transferase, mu 1	0,59	0,0146
1446524_at	NA	NA	0,59	0,0014
1420930_s_at	Ctnnal1	catenin (cadherin associated protein), alpha-like 1	0,59	0,0158
1435280_at	AI452195	expressed sequence AI452195	0,59	0,0004
1454647_at	Nphp3	nephronophthisis 3 (adolescent)	0,59	0,0486
1433856_at	Hisppd1	histidine acid phosphatase domain containing 1	0,59	0,0248
1454858_x_at	Mettl7a1	methyltransferase like 7A1	0,59	0,0010
1447774_x_at	5730469M10Rik	RIKEN cDNA 5730469M10 gene	0,59	0,0056
1421312_a_at	Kifc2	kinesin family member C2	0,59	0,0029
1456480_at	Fry	furry homolog (Drosophila)	0,59	0,0164
1455765_a_at	Abcc8	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	0,59	0,0114
1429809_at	Tmtc2	transmembrane and tetratricopeptide repeat containing 2	0,59	0,0365
1428662_a_at	Hopx	HOP homeobox	0,59	0,0044
1425837_a_at	Ccrn4l	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	0,59	0,0482
1435787_at	Ppm1l	protein phosphatase 1 (formerly 2C)-like	0,59	0,0002
1423893_x_at	Apbb1	amyloid beta (A4) precursor protein-binding, family B, member 1	0,59	0,0217
1449834_at	Magix	MAGI family member, X-linked	0,60	0,0215
1428344_at	Ppapdc2	phosphatidic acid phosphatase type 2 domain containing 2	0,60	0,0031
1429918_at	Arhgap20	Rho GTPase activating protein 20	0,60	0,0328
1422589_at	Rab3a	RAB3A, member RAS oncogene family	0,60	0,0306
1449544_a_at	Kcnh2	potassium voltage-gated channel, subfamily H (eag-related), member 2	0,60	0,0399
1420619_a_at	Aes	amino-terminal enhancer of split	0,60	0,0053
1452939_a_at	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	0,60	0,0309
1418589_a_at	Mlf1	myeloid leukemia factor 1	0,60	0,0025
1450933_at	Pde7a	phosphodiesterase 7A	0,60	0,0383
1417190_at	Nampt	nicotinamide phosphoribosyltransferase	0,60	0,0015
1456716_s_at	3110002H16Rik	RIKEN cDNA 3110002H16 gene	0,60	0,0034
1454803_a_at	Hdac11	histone deacetylase 11	0,60	0,0095
1424175_at	Tef	thyrotroph embryonic factor	0,60	0,0350
1422948_s_at	Hist1h3a	histone cluster 1, H3a	0,60	0,0001

1455320_at	NA	NA	0,60	0,0017
1452798_s_at	Mapk1ip1	mitogen-activated protein kinase 1 interacting protein 1	0,60	0,0235
1417169_at	Usp2	ubiquitin specific peptidase 2	0,60	0,0192
1435630_s_at	Acat2	acetyl-Coenzyme A acetyltransferase 2	0,60	0,0006
1448717_at	Gcdh	glutaryl-Coenzyme A dehydrogenase	0,60	0,0004
1428731_at	Usp54	ubiquitin specific peptidase 54	0,60	0,0082
1417405_at	Stard3	START domain containing 3	0,60	0,0010
1427052_at	Acacb	acetyl-Coenzyme A carboxylase beta	0,60	0,0002
1435096_at	Ric8b	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)	0,60	0,0006
1417841_at	Pxmp2	peroxisomal membrane protein 2	0,60	0,0054
1451776_s_at	Hopx	HOP homeobox	0,60	0,0070
1459793_s_at	Lyrm5	LYR motif containing 5	0,60	0,0033
1422221_at	Hand2	heart and neural crest derivatives expressed transcript 2	0,61	0,0111
1436568_at	Jam2	junction adhesion molecule 2	0,61	0,0104
1448181_at	Klf15	Kruppel-like factor 15	0,61	0,0494
1452716_at	5730469M10Rik	RIKEN cDNA 5730469M10 gene	0,61	0,0013
1427287_s_at	Itpr2	inositol 1,4,5-triphosphate receptor 2	0,61	0,0038
1454840_at	Mccc2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	0,61	0,0023
1454935_at	D930001I22Rik	RIKEN cDNA D930001I22 gene	0,61	0,0003
1435893_at	Vldlr	very low density lipoprotein receptor	0,61	0,0005
1424670_s_at	Zfyve21	zinc finger, FYVE domain containing 21	0,61	0,0005
1438980_x_at	Pm20d1	peptidase M20 domain containing 1	0,61	0,0048
1435365_at	4732415M23Rik	RIKEN cDNA 4732415M23 gene	0,61	0,0115
1429206_at	Rhobtb1	Rho-related BTB domain containing 1	0,61	0,0415
1452833_at	Rapgef2	Rap guanine nucleotide exchange factor (GEF) 2	0,61	0,0059
1441679_at	NA	NA	0,61	0,0383
1418485_at	Slc4a3	solute carrier family 4 (anion exchanger), member 3	0,61	0,0164
1452685_at	0610009O20Rik	RIKEN cDNA 0610009O20 gene	0,61	0,0072
1431028_a_at	Pank1	pantothenate kinase 1	0,61	0,0094
1445873_at	Tfdp2	transcription factor Dp 2	0,61	0,0312
1452457_a_at	Prkab1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	0,61	0,0132
1424510_at	Nudt6	nudix (nucleoside diphosphate linked moiety X)-type motif 6	0,61	0,0040
1432445_at	2310016G11Rik	RIKEN cDNA 2310016G11 gene	0,61	0,0087
1428151_x_at	Ccbl1	cysteine conjugate-beta lyase 1	0,61	0,0019
1423145_a_at	Tcap	titin-cap	0,61	0,0180
1428996_at	4833426J09Rik	RIKEN cDNA 4833426J09 gene	0,61	0,0118
1429339_a_at	Acad10	acyl-Coenzyme A dehydrogenase family, member 10	0,62	0,0013
1452538_at	Igh-6	immunoglobulin heavy chain 6 (heavy chain of IgM)	0,62	0,0296
1429681_a_at	Gpsn2	glycoprotein, synaptic 2	0,62	0,0028
1423713_at	Abcb8	ATP-binding cassette, sub-family B (MDR/TAP), member 8	0,62	0,0088
1434170_at	Wdr40b	WD repeat domain 40B	0,62	0,0050
1437498_at	ENSMUSG00000055440	predicted gene, ENSMUSG00000055440	0,62	0,0026
1435750_at	Gchfr	GTP cyclohydrolase I feedback regulator	0,62	0,0002
1429064_at	Dip2c	DIP2 disco-interacting protein 2 homolog C (Drosophila)	0,62	0,0000
1419039_at	Cyp2d22	cytochrome P450, family 2, subfamily d, polypeptide 22	0,62	0,0165

1427153_at	Bckdhb	branched chain ketoacid dehydrogenase E1, beta polypeptide	0,62	0,0009
1453750_x_at	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	0,62	0,0122
1435066_at	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	0,62	0,0007
1430477_s_at	NA	NA	0,62	0,0121
1416958_at	Nr1d2	nuclear receptor subfamily 1, group D, member 2	0,62	0,0187
1436219_at	4933403F05Rik	RIKEN cDNA 4933403F05 gene	0,62	0,0072
1437269_at	Ttc38	tetratricopeptide repeat domain 38	0,62	0,0058
1452204_at	Anks1	ankyrin repeat and SAM domain containing 1	0,62	0,0009
1415911_at	Impact	imprinted and ancient	0,62	0,0145
1419577_at	Fig4	FIG4 homolog (S. cerevisiae)	0,62	0,0019
1441185_at	Msi2	Musashi homolog 2 (Drosophila)	0,62	0,0314
1451501_a_at	Ghr	growth hormone receptor	0,62	0,0333
1450665_at	Gabpa	GA repeat binding protein, alpha	0,62	0,0142
1419455_at	Il10rb	interleukin 10 receptor, beta	0,62	0,0018
1448136_at	Enpp2	ectonucleotide pyrophosphatase/phosphodiesterase 2	0,62	0,0046
1417542_at	Rps6ka2	ribosomal protein S6 kinase, polypeptide 2	0,62	0,0161
1426502_s_at	Gpt	glutamic pyruvic transaminase, soluble	0,62	0,0415
1422309_a_at	Lenep	lens epithelial protein	0,62	0,0035
1424485_at	Angptl3	angiopoietin-like 3	0,62	0,0183
1447739_x_at	Klhdc4	kelch domain containing 4	0,62	0,0065
1422264_s_at	Klf9	Kruppel-like factor 9	0,62	0,0080
1455376_at	1300010F03Rik	RIKEN cDNA 1300010F03 gene	0,62	0,0018
1452353_at	Gpr155	G protein-coupled receptor 155	0,62	0,0018
1417883_at	Gstt2	glutathione S-transferase, theta 2	0,62	0,0052
1447673_x_at	1700015C15Rik	RIKEN cDNA 1700015C15 gene	0,62	0,0023
1438641_x_at	Fam57b	family with sequence similarity 57, member B	0,62	0,0199
1418238_at	Ivd	isovaleryl coenzyme A dehydrogenase	0,63	0,0022
1434581_at	2410066E13Rik	RIKEN cDNA 2410066E13 gene	0,63	0,0356
1435841_s_at	Suclg2	succinate-Coenzyme A ligase, GDP-forming, beta subunit	0,63	0,0001
1428804_at	Mfap3l	microfibrillar-associated protein 3-like	0,63	0,0023
1428014_at	Hist1h4h	histone cluster 1, H4h	0,63	0,0074
1419292_at	Htra3	HtrA serine peptidase 3	0,63	0,0143
1427074_at	Pcmtd2	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	0,63	0,0131
1428081_at	Klhl21	kelch-like 21 (Drosophila)	0,63	0,0001
1450643_s_at	Acsl1	acyl-CoA synthetase long-chain family member 1	0,63	0,0146
1446738_at	NA	NA	0,63	0,0038
1447760_x_at	Ehf	ets homologous factor	0,63	0,0254
1421126_at	Ryr2	ryanodine receptor 2, cardiac	0,63	0,0404
1428614_at	Ldhd	lactate dehydrogenase D	0,63	0,0002
1455531_at	Mfsd4	major facilitator superfamily domain containing 4	0,63	0,0030
1460254_at	1810049H13Rik	RIKEN cDNA 1810049H13 gene	0,63	0,0275
1428519_at	2610528E23Rik	RIKEN cDNA 2610528E23 gene	0,63	0,0331
1428025_s_at	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	0,63	0,0313
1433873_s_at	Pcnt	pericentrin (kendrin)	0,63	0,0324
1449076_x_at	Adi1	acireductone dioxygenase 1	0,63	0,0015
1436739_at	Agtr1a	angiotensin II receptor, type 1a	0,63	0,0207
1423104_at	Irs1	insulin receptor substrate 1	0,63	0,0231
1439675_at	Ppara	peroxisome proliferator activated receptor alpha	0,63	0,0030

1460279_a_at	Gtf2i	general transcription factor II I	0,63	0,0100
1430776_s_at	Ankrd24	ankyrin repeat domain 24	0,63	0,0454
1434133_s_at	Wdr42a	WD repeat domain 42A	0,63	0,0034
1445431_at	NA	NA	0,63	0,0040
1434013_at	Ablim3	actin binding LIM protein family, member 3	0,64	0,0293
1455558_at	Ncrna00153	non-protein coding RNA 153	0,64	0,0017
1438195_at	Gpd1l	glycerol-3-phosphate dehydrogenase 1-like	0,64	0,0017
1433493_at	Fam73b	family with sequence similarity 73, member B	0,64	0,0289
1424833_at	Itpr2	inositol 1,4,5-triphosphate receptor 2	0,64	0,0015
1450660_at	Pts	6-pyruvoyl-tetrahydropterin synthase	0,64	0,0064
1451050_at	Nt5c3	5'-nucleotidase, cytosolic III	0,64	0,0109
1424308_at	Slc24a3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	0,64	0,0067
1454967_at	NA	NA	0,64	0,0009
1416301_a_at	Ebf1	early B-cell factor 1	0,64	0,0187
1426729_at	Fam131a	family with sequence similarity 131, member A	0,64	0,0026
1451019_at	Ctsf	cathepsin F	0,64	0,0241
1452707_at	Klhl30	kelch-like 30 (Drosophila)	0,64	0,0014
1418093_a_at	Egf	epidermal growth factor	0,64	0,0111
1421180_at	Lix1	limb expression 1 homolog (chicken)	0,64	0,0307
1434832_at	Foxo3	forkhead box O3	0,64	0,0247
1417673_at	Grb14	growth factor receptor bound protein 14	0,64	0,0094
1424882_a_at	Nt5dc2	5'-nucleotidase domain containing 2	0,64	0,0303
1449969_at	Tmod4	tropomodulin 4	0,64	0,0471
1435292_at	Tbc1d4	TBC1 domain family, member 4	0,64	0,0089
1460601_at	Myrip	myosin VIIA and Rab interacting protein	0,64	0,0044
1417928_at	Pdlim4	PDZ and LIM domain 4	0,64	0,0032
1427441_a_at	Suclg2	succinate-Coenzyme A ligase, GDP-forming, beta subunit	0,64	0,0111
1430527_a_at	Rnf167	ring finger protein 167	0,64	0,0279
1415958_at	Slc2a4	solute carrier family 2 (facilitated glucose transporter), member 4	0,64	0,0199
1437462_x_at	Mmp15	matrix metallopeptidase 15	0,64	0,0386
1429965_at	Lonrf2	LON peptidase N-terminal domain and ring finger 2	0,64	0,0012
1433486_at	Clcn3	chloride channel 3	0,64	0,0033
1436991_x_at	Gsn	gelsolin	0,64	0,0001
1434235_at	Slc20a2	solute carrier family 20, member 2	0,64	0,0012
1433805_at	Jak1	Janus kinase 1	0,64	0,0196
1454002_at	NA	NA	0,64	0,0037
1436644_x_at	Tmem25	transmembrane protein 25	0,64	0,0151
1424062_at	Ube2d1	ubiquitin-conjugating enzyme E2D 1, UBC4/5 homolog (yeast)	0,64	0,0105
1438338_at	Mdh1	malate dehydrogenase 1, NAD (soluble)	0,65	0,0022
1419405_at	Nmb	neuromedin B	0,65	0,0409
1451226_at	Pex6	peroxisomal biogenesis factor 6	0,65	0,0164
1428613_at	Ldhd	lactate dehydrogenase D	0,65	0,0002
1451528_at	Tmem82	transmembrane protein 82	0,65	0,0080
1424119_at	Prkab1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	0,65	0,0001
1418502_a_at	Oxr1	oxidation resistance 1	0,65	0,0412
1437496_at	Acad10	acyl-Coenzyme A dehydrogenase family, member 10	0,65	0,0088
1434273_at	Fam174b	family with sequence similarity 174, member B	0,65	0,0163
1448370_at	Ulk1	Unc-51 like kinase 1 (C. elegans)	0,65	0,0024
1460112_at	NA	NA	0,65	0,0015
1416798_a_at	Nme4	non-metastatic cells 4, protein expressed in	0,65	0,0330

1457894_at	Mettl11b	methyltransferase like 11B	0,65	0,0476
1439793_at	Gja3	gap junction protein, alpha 3	0,65	0,0028
1448612_at	Sfn	stratifin	0,65	0,0455
1421086_at	Per3	period homolog 3 (Drosophila)	0,65	0,0244
1455492_at	B330016D10Rik	RIKEN cDNA B330016D10 gene	0,65	0,0397
1452020_a_at	Siva1	SIVA1, apoptosis-inducing factor	0,65	0,0021
1435275_at	Cox6b2	cytochrome c oxidase subunit VIb polypeptide 2	0,65	0,0267
1430421_a_at	Tmem205	transmembrane protein 205	0,65	0,0011
1433782_at	Cldn12	claudin 12	0,65	0,0046
1440343_at	Rps6ka5	ribosomal protein S6 kinase, polypeptide 5	0,65	0,0055
1452807_s_at	Fam57b	family with sequence similarity 57, member B	0,65	0,0054
1449377_at	Nicn1	nicolin 1	0,65	0,0426
1424400_a_at	Aldh1l1	aldehyde dehydrogenase 1 family, member L1	0,65	0,0256
1449964_a_at	Mlycd	malonyl-CoA decarboxylase	0,65	0,0330
1459756_at	Cnot10	CCR4-NOT transcription complex, subunit 10	0,65	0,0120
1416772_at	Cpt2	carnitine palmitoyltransferase 2	0,65	0,0043
1422279_at	Fv1	Friend virus susceptibility 1	0,65	0,0462
1437563_at	Phf20l1	PHD finger protein 20-like 1	0,65	0,0333
1421762_at	Kcnj5	potassium inwardly-rectifying channel, subfamily J, member 5	0,65	0,0128
1444085_at	Pdss2	prenyl (solanesyl) diphosphate synthase, subunit 2	0,65	0,0001
1434909_at	Rragd	Ras-related GTP binding D	0,65	0,0026
1454614_at	1810013D10Rik	RIKEN cDNA 1810013D10 gene	0,65	0,0169
1438968_x_at	Spint2	serine protease inhibitor, Kunitz type 2	0,65	0,0026
1420513_at	Efcab2	EF-hand calcium binding domain 2	0,65	0,0007
1452864_at	Med12l	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)-like	0,65	0,0259
1459238_at	NA	NA	0,65	0,0209
1448491_at	Ech1	enoyl coenzyme A hydratase 1, peroxisomal	0,65	0,0008
1423915_at	Olfml2b	olfactomedin-like 2B	0,65	0,0125
1434264_at	Ank2	ankyrin 2, brain	0,65	0,0037
1436590_at	Ppp1r3b	protein phosphatase 1, regulatory (inhibitor) subunit 3B	0,65	0,0493
1439836_at	Asb15	ankyrin repeat and SOCS box-containing 15	0,66	0,0008
1423979_a_at	Slc25a29	solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), member 29	0,66	0,0022
1433711_s_at	Sesn1	sestrin 1	0,66	0,0302
1455590_at	Nqo2	NAD(P)H dehydrogenase, quinone 2	0,66	0,0009
1445307_at	NA	NA	0,66	0,0241
1438183_x_at	Sord	sorbitol dehydrogenase	0,66	0,0132
1447557_at	Rabif	RAB interacting factor	0,66	0,0173
1415812_at	Gsn	gelsolin	0,66	0,0011
1457721_at	Ppara	peroxisome proliferator activated receptor alpha	0,66	0,0028
1452264_at	Tenc1	tensin like C1 domain-containing phosphatase	0,66	0,0184
1416352_s_at	Gpsn2	glycoprotein, synaptic 2	0,66	0,0046
1436795_at	9630058J23Rik	RIKEN cDNA 9630058J23 gene	0,66	0,0005
1450707_at	Doc2g	double C2, gamma	0,66	0,0395
1417962_s_at	Ghr	growth hormone receptor	0,66	0,0001
1418321_at	Dci	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase)	0,66	0,0018
1456293_s_at	Ccnh	cyclin H	0,66	0,0001
1428146_s_at	Acaa2	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	0,66	0,0059
1443854_at	Hand2	heart and neural crest derivatives expressed transcript 2	0,66	0,0324
1423980_at	Slc25a29	solute carrier family 25 (mitochondrial carrier,	0,66	0,0044

		palmitoylcarnitine transporter), member 29		
1455008_at	NA	NA	0,66	0,0005
1438963_s_at	Tfpt	TCF3 (E2A) fusion partner	0,66	0,0171
1437861_s_at	Prkce	protein kinase C, epsilon	0,66	0,0043
1443152_at	Ptcd3	pentatricopeptide repeat domain 3	0,66	0,0132
1448927_at	Kcnn2	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	0,66	0,0144
1416863_at	Abhd8	abhydrolase domain containing 8	0,66	0,0087
1436168_at	C730029A08Rik	RIKEN cDNA C730029A08 gene	0,66	0,0433
1451974_at	Osbpl2	oxysterol binding protein-like 2	0,66	0,0003
1448900_at	D16H22S680E	DNA segment, Chr 16, human D22S680E, expressed	0,66	0,0006
1428289_at	2310051E17Rik	RIKEN cDNA 2310051E17 gene	0,66	0,0028
1452375_at	Aldh4a1	aldehyde dehydrogenase 4 family, member A1	0,66	0,0338
1434140_at	Mcf2l	mcf.2 transforming sequence-like	0,66	0,0243
1455785_at	Kcna1	potassium voltage-gated channel, shaker-related subfamily, member 1	0,66	0,0271
1442416_at	D930001B02	hypothetical protein D930001B02	0,66	0,0311
1436050_x_at	Hes6	hairy and enhancer of split 6 (Drosophila)	0,66	0,0041
1436121_a_at	Nsmce1	non-SMC element 1 homolog (S. cerevisiae)	0,66	0,0105
1449130_at	Cd1d1	CD1d1 antigen	0,66	0,0057
1454645_at	Mgrn1	mahogunin, ring finger 1	0,66	0,0140
1454741_s_at	Tmem164	transmembrane protein 164	0,66	0,0437
1416609_at	BC004004	cDNA sequence BC004004	0,66	0,0013
1428145_at	Acaa2	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	0,67	0,0014
1453173_at	2310005E10Rik	RIKEN cDNA 2310005E10 gene	0,67	0,0099
1427577_x_at	Igk	immunoglobulin kappa chain complex	0,67	0,0288
1416105_at	Nnt	nicotinamide nucleotide transhydrogenase	0,67	0,0021
1418865_at	Zfp385a	zinc finger protein 385A	0,67	0,0173
1419062_at	Epb4.1l3	erythrocyte protein band 4.1-like 3	0,67	0,0075
1421469_a_at	Stat5a	signal transducer and activator of transcription 5A	0,67	0,0011
1424076_at	Gdpd1	glycerophosphodiester phosphodiesterase domain containing 1	0,67	0,0015
1448839_at	Kank3	KN motif and ankyrin repeat domains 3	0,67	0,0485
1440118_at	Slc25a39	solute carrier family 25, member 39	0,67	0,0341
1436146_at	4930481A15Rik	RIKEN cDNA 4930481A15 gene	0,67	0,0370
1441878_s_at	1810049H13Rik	RIKEN cDNA 1810049H13 gene	0,67	0,0483
1456753_at	NA	NA	0,67	0,0019
1451559_a_at	Dhrs4	dehydrogenase/reductase (SDR family) member 4	0,67	0,0047
1431697_at	Synj2	synaptojanin 2	0,67	0,0289
1428512_at	Bhlhb9	basic helix-loop-helix domain containing, class B9	0,67	0,0043
1418706_at	Slc38a3	solute carrier family 38, member 3	0,67	0,0034
1433533_x_at	Prkag1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	0,67	0,0156
1424480_s_at	Akt2	thymoma viral proto-oncogene 2	0,67	0,0011
1423611_at	Alpl	alkaline phosphatase, liver/bone/kidney	0,67	0,0071
1455991_at	Ccbl2	cysteine conjugate-beta lyase 2	0,67	0,0334
1428695_at	Sdr39u1	short chain dehydrogenase/reductase family 39U, member 1	0,67	0,0417
1441988_at	Ppm1k	protein phosphatase 1K (PP2C domain containing)	0,67	0,0119
1443739_at	NA	NA	0,67	0,0425

1456885_at	NA	NA	0,67	0,0031
1420631_a_at	Blcap	bladder cancer associated protein homolog (human)	0,67	0,0006
1415818_at	Anxa6	annexin A6	0,67	0,0424
1450492_at	Cngb3	cyclic nucleotide gated channel beta 3	0,67	0,0118
1417008_at	Crat	carnitine acetyltransferase	0,67	0,0005
1433717_at	D19Wsu162e	DNA segment, Chr 19, Wayne State University 162, expressed	0,67	0,0001
1429766_at	2810013P06Rik	RIKEN cDNA 2810013P06 gene	0,67	0,0312
1428524_at	Cars2	cysteinyl-tRNA synthetase 2 (mitochondrial)(putative)	0,67	0,0297
1446288_at	C78692	expressed sequence C78692	0,67	0,0170
1417211_a_at	1110032A03Rik	RIKEN cDNA 1110032A03 gene	0,67	0,0389
1440234_at	1810012P15Rik	RIKEN cDNA 1810012P15 gene	0,67	0,0041
1452111_at	Mrps35	mitochondrial ribosomal protein S35	0,67	0,0010
1455961_at	NA	NA	0,67	0,0214
1418377_a_at	Siva1	SIVA1, apoptosis-inducing factor	0,67	0,0027
1460635_at	Fastk	Fas-activated serine/threonine kinase	0,67	0,0026
1438915_at	6720401G13Rik	RIKEN cDNA 6720401G13 gene	0,67	0,0138
1460703_at	Ascc1	activating signal cointegrator 1 complex subunit 1	0,67	0,0125
1424490_at	Zfp428	zinc finger protein 428	0,67	0,0005
1438251_x_at	Htra1	HtrA serine peptidase 1	0,67	0,0492
1425627_x_at	Gstm1	glutathione S-transferase, mu 1	0,67	0,0241
1456629_at	Kank3	KN motif and ankyrin repeat domains 3	0,67	0,0181
1456616_a_at	Bsg	basigin	0,67	0,0177
1427542_at	Sobp	sine oculis-binding protein homolog (Drosophila)	0,68	0,0020
1416383_a_at	Pcx	pyruvate carboxylase	0,68	0,0085
1437866_at	Dusp18	dual specificity phosphatase 18	0,68	0,0287
1426427_at	Ttll1	tubulin tyrosine ligase-like 1	0,68	0,0177
1453135_at	Fndc5	fibronectin type III domain containing 5	0,68	0,0438
1433827_at	Atp8a1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	0,68	0,0481
1434151_at	Mettl7a1	methyltransferase like 7A1	0,68	0,0008
1447655_x_at	Sox6	SRY-box containing gene 6	0,68	0,0174
1438010_at	Tmem201	transmembrane protein 201	0,68	0,0340
1444305_at	Myh7b	myosin, heavy chain 7B, cardiac muscle, beta	0,68	0,0303
1424834_s_at	Itpr2	inositol 1,4,5-triphosphate receptor 2	0,68	0,0274
1433931_at	C030046I01Rik	RIKEN cDNA C030046I01 gene	0,68	0,0095
1420150_at	Spsb1	splA/ryanodine receptor domain and SOCS box containing 1	0,68	0,0058
1458425_at	NA	NA	0,68	0,0010
1454974_at	Ntn1	netrin 1	0,68	0,0034
1450932_s_at	Dock9	dedicator of cytokinesis 9	0,68	0,0008
1438910_a_at	Stom	stomatin	0,68	0,0042
1419805_s_at	LOC100045315	similar to Ggps1 protein	0,68	0,0384
1452464_a_at	Metapl1	methionine aminopeptidase-like 1	0,68	0,0300
1446833_at	NA	NA	0,68	0,0011
1423707_at	Tmem50b	transmembrane protein 50B	0,68	0,0016
1448602_at	Pygm	muscle glycogen phosphorylase	0,68	0,0211
1428647_at	Pbx1	pre B-cell leukemia transcription factor 1	0,68	0,0014
1416412_at	Nsmaf	neutral sphingomyelinase (N-SMase) activation associated factor	0,68	0,0043
1449331_a_at	Rapsn	receptor-associated protein of the synapse	0,68	0,0321

1417049_at	Rhd	Rh blood group, D antigen	0,68	0,0003
1439509_at	2900008C10Rik	RIKEN cDNA 2900008C10 gene	0,68	0,0007
1418782_at	Rxrg	retinoid X receptor gamma	0,68	0,0005
1449151_at	Pctk3	PCTAIRE-motif protein kinase 3	0,68	0,0018
1452666_a_at	Tmcc2	transmembrane and coiled-coil domains 2	0,68	0,0009
1417311_at	Crip2	cysteine rich protein 2	0,68	0,0003
1426493_a_at	Kifc2	kinesin family member C2	0,68	0,0256
1456943_a_at	Dbndd2	dysbindin (dystrobrevin binding protein 1) domain containing 2	0,68	0,0158
1428651_at	Klhl24	kelch-like 24 (Drosophila)	0,68	0,0038
1458350_at	Opa3	optic atrophy 3 (human)	0,68	0,0076
1427251_at	Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	0,68	0,0075
1436500_at	Rps24	ribosomal protein S24	0,68	0,0176
1460192_at	Osbpl1a	oxysterol binding protein-like 1A	0,68	0,0016
1450395_at	Slc22a5	solute carrier family 22 (organic cation transporter), member 5	0,68	0,0047
1443575_at	2310040G24Rik	RIKEN cDNA 2310040G24 gene	0,68	0,0231
1416610_a_at	Clcn3	chloride channel 3	0,68	0,0026
1425050_at	Isoc1	isochorismatase domain containing 1	0,68	0,0003
1453216_at	Gpt	glutamic pyruvic transaminase, soluble	0,68	0,0011
1426994_at	Phlpp	PH domain and leucine rich repeat protein phosphatase	0,68	0,0006
1435714_x_at	Il17d	interleukin 17D	0,68	0,0472
1418284_at	Vps72	vacuolar protein sorting 72 (yeast)	0,68	0,0028
1448143_at	Aldh2	aldehyde dehydrogenase 2, mitochondrial	0,68	0,0165
1428382_at	Smarcc2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	0,68	0,0175
1451372_a_at	Art1	ADP-ribosyltransferase 1	0,68	0,0034
1428338_at	Spata2L	spermatogenesis associated 2-like	0,68	0,0221
1455702_at	Wdr22	WD repeat domain 22	0,68	0,0358
1451543_at	Fbxo21	F-box protein 21	0,68	0,0247
1448539_a_at	Acy3	aspartoacylase (aminoacylase) 3	0,68	0,0065
1448870_at	Ltbp1	latent transforming growth factor beta binding protein 1	0,68	0,0014
1448104_at	Aldh6a1	aldehyde dehydrogenase family 6, subfamily A1	0,68	0,0004
1455759_a_at	Ankhd1	ankyrin repeat and KH domain containing 1	0,68	0,0070
1417408_at	F3	coagulation factor III	0,68	0,0110
1422187_at	Gabrg3	gamma-aminobutyric acid (GABA-A) receptor, subunit gamma 3	0,69	0,0115
1455061_a_at	Acaa2	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	0,69	0,0382
1451500_at	Ushbp1	Usher syndrome 1C binding protein 1	0,69	0,0177
1423314_s_at	Pde7a	phosphodiesterase 7A	0,69	0,0457
1419416_a_at	Rarg	retinoic acid receptor, gamma	0,69	0,0083
1419646_a_at	Mbp	myelin basic protein	0,69	0,0144
1420762_a_at	Ybx2	Y box protein 2	0,69	0,0448
1424505_at	Rmnd1	required for meiotic nuclear division 1 homolog (S. cerevisiae)	0,69	0,0485
1416608_a_at	BC004004	cDNA sequence BC004004	0,69	0,0045
1434276_x_at	BC004004	cDNA sequence BC004004	0,69	0,0035
1449314_at	Zfpm2	zinc finger protein, multitype 2	0,69	0,0106
1448391_at	Rab9	RAB9, member RAS oncogene family	0,69	0,0489
1435917_at	Ociad2	OCIA domain containing 2	0,69	0,0312
1434265_s_at	Ank2	ankyrin 2, brain	0,69	0,0007
1438916_x_at	6720401G13Rik	RIKEN cDNA 6720401G13 gene	0,69	0,0072

1419097_a_at	Stom	stomatin	0,69	0,0202
1420640_at	Jmy	junction-mediating and regulatory protein	0,69	0,0372
1451890_at	Kif13a	kinesin family member 13A	0,69	0,0494
1425788_a_at	Echdc2	enoyl Coenzyme A hydratase domain containing 2	0,69	0,0462
1436926_at	Esrrb	estrogen related receptor, beta	0,69	0,0378
AFFX-PyruCarbMur/L09192_3_at	Pcx	pyruvate carboxylase	0,69	0,0025
1447823_x_at	Mapk12	mitogen-activated protein kinase 12	0,69	0,0140
1452335_at	Mfsd8	major facilitator superfamily domain containing 8	0,69	0,0058
1425051_at	Isoc1	isochorismatase domain containing 1	0,69	0,0044
1425529_s_at	D19Wsu162e	DNA segment, Chr 19, Wayne State University 162, expressed	0,69	0,0141
1423365_at	Cacna1g	calcium channel, voltage-dependent, T type, alpha 1G subunit	0,69	0,0341
1420519_a_at	Eral1	Era (G-protein)-like 1 (E. coli)	0,69	0,0189
1451148_at	Pink1	PTEN induced putative kinase 1	0,69	0,0275
1459072_at	NA	NA	0,69	0,0048
1416411_at	Gstm2	glutathione S-transferase, mu 2	0,69	0,0234
1450884_at	Cd36	CD36 antigen	0,69	0,0009
1437171_x_at	Gsn	gelsolin	0,69	0,0004
1433817_at	Agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	0,69	0,0241
1422064_a_at	Zbtb20	zinc finger and BTB domain containing 20	0,69	0,0095
1417129_a_at	Meis2	Meis homeobox 2	0,69	0,0359
1452962_at	Tmem25	transmembrane protein 25	0,69	0,0124
1426822_at	Rhot2	ras homolog gene family, member T2	0,69	0,0008
1434441_at	1110018J18Rik	RIKEN cDNA 1110018J18 gene	0,69	0,0009
1451965_at	LOC672450	V(kappa) gene product	0,69	0,0280
1434141_at	Gucy1a3	guanylate cyclase 1, soluble, alpha 3	0,69	0,0234
1436070_at	Glo1	glyoxalase 1	0,69	0,0336
1433541_a_at	Ubap2l	ubiquitin associated protein 2-like	0,69	0,0378
1418983_at	Inadl	InaD-like (Drosophila)	0,69	0,0073
1427656_at	Tcrb-J	T-cell receptor beta, joining region	0,69	0,0461
1440475_at	AW011738	expressed sequence AW011738	0,70	0,0288
1451085_at	C030006K11Rik	RIKEN cDNA C030006K11 gene	0,70	0,0116
1445315_at	NA	NA	0,70	0,0203
1426440_at	Dhrs7	dehydrogenase/reductase (SDR family) member 7	0,70	0,0154
1452021_a_at	Hes6	hairy and enhancer of split 6 (Drosophila)	0,70	0,0213
1422522_at	Fxr2	fragile X mental retardation, autosomal homolog 2	0,70	0,0211
1456072_at	Ppp1r9a	protein phosphatase 1, regulatory (inhibitor) subunit 9A	0,70	0,0011
1454987_a_at	H2-Ke6	H2-K region expressed gene 6	0,70	0,0049
1448499_a_at	Ephx2	epoxide hydrolase 2, cytoplasmic	0,70	0,0017
1419471_a_at	Nudc	nuclear distribution gene C homolog (Aspergillus)	0,70	0,0015
1425678_a_at	Snrk	SNF related kinase	0,70	0,0274
1451523_a_at	Mif4gd	MIF4G domain containing	0,70	0,0018
1451088_a_at	Oxa1l	oxidase assembly 1-like	0,70	0,0023
1460076_x_at	NA	NA	0,70	0,0225
1429024_at	Rbm20	RNA binding motif protein 20	0,70	0,0197
1449118_at	Dbt	dihydrolipoamide branched chain transacylase E2	0,70	0,0126
1417324_at	Mast2	microtubule associated serine/threonine kinase 2	0,70	0,0118
1428323_at	Gpd2	glycerol phosphate dehydrogenase 2, mitochondrial	0,70	0,0478
1435417_at	AI464131	expressed sequence AI464131	0,70	0,0008
1423269_a_at	Nedd4l	neural precursor cell expressed, developmentally down-	0,70	0,0211

		regulated gene 4-like		
1452988_at	2610306M01Rik	RIKEN cDNA 2610306M01 gene	0,70	0,0208
1428290_at	Mipep	mitochondrial intermediate peptidase	0,70	0,0025
1449620_s_at	Adcy9	adenylate cyclase 9	0,70	0,0470
1451405_at	Pcca	propionyl-Coenzyme A carboxylase, alpha polypeptide	0,70	0,0015
1427427_at	Ryr3	ryanodine receptor 3	0,70	0,0227
1439802_at	Stk35	serine/threonine kinase 35	0,70	0,0177
1424845_a_at	Cep68	centrosomal protein 68	0,70	0,0100
1424455_at	Gprasp1	G protein-coupled receptor associated sorting protein 1	0,70	0,0142
1438505_s_at	Rnasen	ribonuclease III, nuclear	0,70	0,0267
1418146_a_at	Rbl2	retinoblastoma-like 2	0,70	0,0299
1418181_at	Ptp4a3	protein tyrosine phosphatase 4a3	0,70	0,0215
1438006_at	4933439F18Rik	RIKEN cDNA 4933439F18 gene	0,70	0,0029
1451279_at	Erc1	ELKS/RAB6-interacting/CAST family member 1	0,70	0,0013
1422728_at	Inha	inhibin alpha	0,70	0,0124
1437494_at	Mapkapk3	mitogen-activated protein kinase-activated protein kinase 3	0,70	0,0033
1428957_at	Tmem177	transmembrane protein 177	0,70	0,0308
1443486_at	Cog7	component of oligomeric golgi complex 7	0,70	0,0069
1435752_s_at	Abcc9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	0,70	0,0016
1416449_x_at	Stxbp2	syntaxin binding protein 2	0,70	0,0482
1423981_x_at	Slc25a29	solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), member 29	0,70	0,0055
1418584_at	Ccnh	cyclin H	0,70	0,0004
1451143_at	1110006G06Rik	RIKEN cDNA 1110006G06 gene	0,70	0,0118
1417775_at	Polr1a	polymerase (RNA) I polypeptide A	0,70	0,0022
1417701_at	Ppp1r14c	protein phosphatase 1, regulatory (inhibitor) subunit 14c	0,70	0,0066
1416824_at	B230118H07Rik	RIKEN cDNA B230118H07 gene	0,70	0,0007
1423447_at	Clpx	caseinolytic peptidase X (E.coli)	0,70	0,0459
1456542_s_at	Qrsl1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	0,70	0,0051
1454137_s_at	Hfe2	hemochromatosis type 2 (juvenile) (human homolog)	0,70	0,0331
1430299_at	Tsc22d4	TSC22 domain family, member 4	0,70	0,0292
1451834_at	Cacnb1	calcium channel, voltage-dependent, beta 1 subunit	0,70	0,0184
1429723_at	6330409N04Rik	RIKEN cDNA 6330409N04 gene	0,70	0,0112
1434908_at	Scaf1	SR-related CTD-associated factor 1	0,70	0,0103
1426323_x_at	Siva1	SIVA1, apoptosis-inducing factor	0,70	0,0034
1424182_at	Acat1	acetyl-Coenzyme A acetyltransferase 1	0,70	0,0236
1451625_a_at	C8g	complement component 8, gamma polypeptide	0,70	0,0324
1432562_at	1110006G14Rik	RIKEN cDNA 1110006G14 gene	0,70	0,0054
1448193_at	5730403B10Rik	RIKEN cDNA 5730403B10 gene	0,70	0,0294
1429071_at	Me3	malic enzyme 3, NADP(+)-dependent, mitochondrial	0,70	0,0095
1428364_at	Scnm1	sodium channel modifier 1	0,70	0,0003
1417003_at	0610012G03Rik	RIKEN cDNA 0610012G03 gene	0,71	0,0126
1457976_at	2010002M12Rik	RIKEN cDNA 2010002M12 gene	0,71	0,0368
1421659_at	Adra1a	adrenergic receptor, alpha 1a	0,71	0,0038
1453487_at	Dhdh	dihydrodiol dehydrogenase (dimeric)	0,71	0,0232
1424786_s_at	Wdr45	WD repeat domain 45	0,71	0,0024

1423806_at	Ints4	integrator complex subunit 4	0,71	0,0064
1455418_at	NA	NA	0,71	0,0313
1431833_a_at	Hmgcs2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	0,71	0,0479
1449093_at	Ctf1	cardiotrophin 1	0,71	0,0148
1425052_at	Isoc1	isochorismatase domain containing 1	0,71	0,0002
1415948_at	Creg1	cellular repressor of E1A-stimulated genes 1	0,71	0,0269
1456673_at	NA	NA	0,71	0,0341
1416778_at	Sdpr	serum deprivation response	0,71	0,0183
1417734_at	Akap8l	A kinase (PRKA) anchor protein 8-like	0,71	0,0291
1419367_at	Decr1	2,4-dienoyl CoA reductase 1, mitochondrial	0,71	0,0293
1452878_at	Prkce	protein kinase C, epsilon	0,71	0,0013
1455750_at	A230067G21Rik	RIKEN cDNA A230067G21 gene	0,71	0,0169
1460067_at	Ccr2	chemokine (C-C motif) receptor 2	0,71	0,0019
1418187_at	Ramp2	receptor (calcitonin) activity modifying protein 2	0,71	0,0260
1450111_a_at	Nudt8	nudix (nucleoside diphosphate linked moiety X)-type motif 8	0,71	0,0059
1453065_at	Aldh5a1	aldhehyde dehydrogenase family 5, subfamily A1	0,71	0,0176
1425341_at	Kcnk3	potassium channel, subfamily K, member 3	0,71	0,0375
1426208_x_at	Plagl1	pleiomorphic adenoma gene-like 1	0,71	0,0300
1417094_at	Acot7	acyl-CoA thioesterase 7	0,71	0,0399
1429306_at	Lzic	leucine zipper and CTNNBIP1 domain containing	0,71	0,0220
1439244_a_at	Tnrc6a	trinucleotide repeat containing 6a	0,71	0,0180
1422500_at	Idh3a	isocitrate dehydrogenase 3 (NAD+) alpha	0,71	0,0129
1455296_at	Adcy5	adenylate cyclase 5	0,71	0,0034
1451486_at	Slc46a3	solute carrier family 46, member 3	0,71	0,0169
1454136_a_at	4921524J17Rik	RIKEN cDNA 4921524J17 gene	0,71	0,0131
1457675_at	2510002D24Rik	RIKEN cDNA 2510002D24 gene	0,71	0,0023
1446844_at	Chchd7	coiled-coil-helix-coiled-coil-helix domain containing 7	0,71	0,0068
1417294_at	Akr7a5	aldo-keto reductase family 7, member A5 (aflatoxin aldehyde reductase)	0,71	0,0125
1448530_at	Gmpr	guanosine monophosphate reductase	0,71	0,0414
1425053_at	Isoc1	isochorismatase domain containing 1	0,71	0,0264
1424682_at	Gpn3	GPN-loop GTPase 3	0,71	0,0040
1422375_a_at	Art1	ADP-ribosyltransferase 1	0,71	0,0243
1418366_at	Hist2h2aa1	histone cluster 2, H2aa1	0,71	0,0035
1456037_x_at	Preb	prolactin regulatory element binding	0,71	0,0384
1417565_at	Abhd5	abhydrolase domain containing 5	0,71	0,0015
1438177_x_at	LOC100048085	similar to ectonucleoside triphosphate diphosphohydrolase 4	0,71	0,0151
1456312_x_at	Gsn	gelsolin	0,71	0,0007
1421417_s_at	Elac1	elaC homolog 1 (E. coli)	0,71	0,0454
1426984_at	2310067B10Rik	RIKEN cDNA 2310067B10 gene	0,71	0,0007
1443405_at	NA	NA	0,71	0,0197
1434611_at	Rnf123	ring finger protein 123	0,71	0,0061
1426055_a_at	Pigq	phosphatidylinositol glycan anchor biosynthesis, class Q	0,71	0,0315
1450376_at	Mxi1	Max interacting protein 1	0,71	0,0029
1422184_a_at	Ak1	adenylate kinase 1	0,71	0,0015
1455267_at	Esrrg	estrogen-related receptor gamma	0,71	0,0045
1429307_s_at	Lzic	leucine zipper and CTNNBIP1 domain containing	0,71	0,0238
1429146_at	6620401M08Rik	RIKEN cDNA 6620401M08 gene	0,71	0,0185
1436251_at	Pde1c	phosphodiesterase 1C	0,71	0,0320

1460216_at	Acads	acyl-Coenzyme A dehydrogenase, short chain	0,71	0,0018
1417506_at	Gmnn	geminin	0,71	0,0225
1451277_at	Zadh2	zinc binding alcohol dehydrogenase, domain containing 2	0,71	0,0133
1459757_x_at	Cnot10	CCR4-NOT transcription complex, subunit 10	0,71	0,0043
1427075_s_at	Pcmtd2	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	0,71	0,0093
1435551_at	Fhod3	formin homology 2 domain containing 3	0,71	0,0065
1452128_a_at	Brcc3	BRCA1/BRCA2-containing complex, subunit 3	0,71	0,0011
1419173_at	Acy1	aminoacylase 1	0,71	0,0034
1454157_a_at	Pla2g2d	phospholipase A2, group IID	0,71	0,0283
1439433_a_at	Slc35a2	solute carrier family 35 (UDP-galactose transporter), member A2	0,71	0,0196
1423689_a_at	Gpsm1	G-protein signalling modulator 1 (AGS3-like, C. elegans)	0,71	0,0024
1428955_x_at	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	0,71	0,0385
1460352_s_at	Pik3r4	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 4, p150	0,71	0,0088
1447921_at	NA	NA	0,71	0,0184
1447807_s_at	Plekhh1	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1	0,71	0,0033
1416635_at	Smpdl3a	sphingomyelin phosphodiesterase, acid-like 3A	0,71	0,0039
1428288_at	2310051E17Rik	RIKEN cDNA 2310051E17 gene	0,72	0,0264
1428657_at	Rreb1	ras responsive element binding protein 1	0,72	0,0399
1423136_at	Fgf1	fibroblast growth factor 1	0,72	0,0365
1428557_a_at	Ormdl1	ORM1-like 1 (S. cerevisiae)	0,72	0,0029
1453421_at	Srr	serine racemase	0,72	0,0073
1452202_at	Pde2a	phosphodiesterase 2A, cGMP-stimulated	0,72	0,0198
1455845_at	Wscd1	WSC domain containing 1	0,72	0,0407
1456510_x_at	Higd1c	HIG1 domain family, member 1C	0,72	0,0093
1431063_at	Ganc	glucosidase, alpha; neutral C	0,72	0,0213
1432509_at	5033430I15Rik	RIKEN cDNA 5033430I15 gene	0,72	0,0449
1427185_at	Mef2a	myocyte enhancer factor 2A	0,72	0,0004
1417661_at	Rdm1	RAD52 motif 1	0,72	0,0113
1437662_at	Acsm5	acyl-CoA synthetase medium-chain family member 5	0,72	0,0236
1455622_at	Podxl2	podocalyxin-like 2	0,72	0,0199
1426934_at	Nhsl1	NHS-like 1	0,72	0,0325
1451451_at	Gca	grancalcin	0,72	0,0317
1423229_at	Inpp5e	inositol polyphosphate-5-phosphatase E	0,72	0,0017
1441912_x_at	C2	complement component 2 (within H-2S)	0,72	0,0472
1448196_at	Mat2b	methionine adenosyltransferase II, beta	0,72	0,0061
1419869_s_at	Hdlbp	high density lipoprotein (HDL) binding protein	0,72	0,0046
1434592_at	Slc16a10	solute carrier family 16 (monocarboxylic acid transporters), member 10	0,72	0,0425
1448099_at	EG432995	predicted gene, EG432995	0,72	0,0163
1436943_at	Cyb5d2	cytochrome b5 domain containing 2	0,72	0,0369
1453233_s_at	Calr3	calreticulin 3	0,72	0,0224
1452005_at	Dlat	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	0,72	0,0185
1420493_a_at	Pcyt2	phosphate cytidylyltransferase 2, ethanolamine	0,72	0,0021
1420776_a_at	Auh	AU RNA binding protein/enoyl-coenzyme A hydratase	0,72	0,0006
1454708_at	Ablim1	actin-binding LIM protein 1	0,72	0,0005
1420520_x_at	Eral1	Era (G-protein)-like 1 (E. coli)	0,72	0,0084
1455098_a_at	Vtn	vitronectin	0,72	0,0434
1423958_a_at	Ttc33	tetratricopeptide repeat domain 33	0,72	0,0004

1451575_a_at	Nudt3	nudix (nucleotide diphosphate linked moiety X)-type motif 3	0,72	0,0103
1428358_at	1810010M01Rik	RIKEN cDNA 1810010M01 gene	0,72	0,0466
1433654_at	Mgea5	meningioma expressed antigen 5 (hyaluronidase)	0,72	0,0042
1418501_a_at	Oxr1	oxidation resistance 1	0,72	0,0006
1417103_at	Ddt	D-dopachrome tautomerase	0,72	0,0043
1442043_at	Lhfpl4	lipoma HMGIC fusion partner-like protein 4	0,72	0,0289
1451392_at	Elmod3	ELMO/CED-12 domain containing 3	0,72	0,0168
1419109_at	Hrc	histidine rich calcium binding protein	0,72	0,0020
1429516_at	Ubr2	ubiquitin protein ligase E3 component n-recognin 2	0,72	0,0077
1457632_s_at	Meis2	Meis homeobox 2	0,72	0,0446
1423313_at	Pde7a	phosphodiesterase 7A	0,72	0,0467
1455985_x_at	Shmt2	serine hydroxymethyltransferase 2 (mitochondrial)	0,72	0,0181
1430769_s_at	Fam122a	family with sequence similarity 122, member A	0,72	0,0225
1460544_at	Mak10	MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)	0,72	0,0219
1420127_s_at	Ccpg1	cell cycle progression 1	0,72	0,0033
1428656_at	Rnasen	ribonuclease III, nuclear	0,72	0,0060
1429429_s_at	Pcmtd1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	0,72	0,0033
1451334_at	1810009O10Rik	RIKEN cDNA 1810009O10 gene	0,72	0,0038
1437377_a_at	Polrmt	polymerase (RNA) mitochondrial (DNA directed)	0,72	0,0054
1433830_at	Hnrnpa2b1	heterogeneous nuclear ribonucleoprotein A2/B1	0,72	0,0168
1417581_at	Dhodh	dihydroorotate dehydrogenase	0,72	0,0162
1457936_at	Mapk8	mitogen-activated protein kinase 8	0,72	0,0041
1455927_x_at	Nsmce1	non-SMC element 1 homolog (S. cerevisiae)	0,72	0,0443
1452877_at	2700029M09Rik	RIKEN cDNA 2700029M09 gene	0,72	0,0054
1428356_at	Osbp2	oxysterol binding protein 2	0,72	0,0047
1415689_s_at	Zkscan3	zinc finger with KRAB and SCAN domains 3	0,72	0,0254
1449131_s_at	Cd1d1	CD1d1 antigen	0,72	0,0254
1436367_at	NA	NA	0,72	0,0210
1430650_at	Zfp191	zinc finger protein 191	0,72	0,0371
1430849_a_at	Cgrrf1	cell growth regulator with ring finger domain 1	0,72	0,0204
1423679_at	2810432L12Rik	RIKEN cDNA 2810432L12 gene	0,72	0,0083
1455076_a_at	4933424B01Rik	RIKEN cDNA 4933424B01 gene	0,72	0,0298
1447773_x_at	6330409D20Rik	RIKEN cDNA 6330409D20 gene	0,72	0,0151
1419606_a_at	Tnnt1	troponin T1, skeletal, slow	0,73	0,0346
1436634_at	Robo3	roundabout homolog 3 (Drosophila)	0,73	0,0154
1452862_at	Rreb1	ras responsive element binding protein 1	0,73	0,0137
1436925_at	Foxn3	forkhead box N3	0,73	0,0303
1458384_at	NA	NA	0,73	0,0270
1423736_a_at	Dym	dymeclin	0,73	0,0019
1424690_at	5930434B04Rik	RIKEN cDNA 5930434B04 gene	0,73	0,0192
1434105_at	Epm2aip1	EPM2A (laforin) interacting protein 1	0,73	0,0173
1438292_x_at	Adk	adenosine kinase	0,73	0,0026
1455361_at	Dgkb	diacylglycerol kinase, beta	0,73	0,0313
1454855_at	Magi2	membrane associated guanylate kinase, WW and PDZ domain containing 2	0,73	0,0393
1440963_at	Cbfa2t3	core-binding factor, runt domain, alpha subunit 2, translocated to, 3 (human)	0,73	0,0312

1448556_at	Prlr	prolactin receptor	0,73	0,0114
1429083_at	Agl	amylo-1,6-glucosidase, 4-alpha-glucanotransferase	0,73	0,0007
1459090_at	NA	NA	0,73	0,0053
1436244_a_at	Tle2	transducin-like enhancer of split 2, homolog of Drosophila E(spl)	0,73	0,0269
1417854_at	Map2k5	mitogen-activated protein kinase kinase 5	0,73	0,0031
1427312_at	Cmya5	cardiomyopathy associated 5	0,73	0,0069
1427598_at	Snord116	small nucleolar RNA, C/D box 116 cluster	0,73	0,0118
1429767_at	2810013P06Rik	RIKEN cDNA 2810013P06 gene	0,73	0,0053
1448038_at	NA	NA	0,73	0,0065
1423448_at	Rab11b	RAB11B, member RAS oncogene family	0,73	0,0500
1438199_at	AI316807	expressed sequence AI316807	0,73	0,0015
1418472_at	Aspa	aspartoacylase	0,73	0,0373
1419472_s_at	Nudc	nuclear distribution gene C homolog (Aspergillus)	0,73	0,0013
1439062_at	Kbtbd3	kelch repeat and BTB (POZ) domain containing 3	0,73	0,0074
1421097_at	Endog	endonuclease G	0,73	0,0248
1428558_at	Ormdl1	ORM1-like 1 (S. cerevisiae)	0,73	0,0210
1447457_at	NA	NA	0,73	0,0461
1434738_at	Tarsl2	threonyl-tRNA synthetase-like 2	0,73	0,0150
1435801_at	Fktn	fukutin	0,73	0,0034
1445841_at	Lrrc39	leucine rich repeat containing 39	0,73	0,0448
1430614_at	4632415K11Rik	RIKEN cDNA 4632415K11 gene	0,73	0,0294
1444108_at	Dnajc25	DnaJ (Hsp40) homolog, subfamily C , member 25	0,73	0,0381
1453187_at	Ociad2	OCIA domain containing 2	0,73	0,0264
1416615_at	Clpp	caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli)	0,73	0,0003
1433753_x_at	Eral1	Era (G-protein)-like 1 (E. coli)	0,73	0,0029
1435656_at	Gmps	guanine monphosphate synthetase	0,73	0,0417
1456465_at	Slc25a44	solute carrier family 25, member 44	0,73	0,0397
1455446_x_at	Acadsb	acyl-Coenzyme A dehydrogenase, short/branched chain	0,73	0,0049
1456595_x_at	Gh	growth hormone	0,73	0,0273
1423068_at	Ift172	intraflagellar transport 172 homolog (Chlamydomonas)	0,73	0,0040
1453485_s_at	1110005A03Rik	RIKEN cDNA 1110005A03 gene	0,73	0,0102
1435980_x_at	Wnt6	wingless-related MMTV integration site 6	0,73	0,0205
1432410_a_at	Bmp7	bone morphogenetic protein 7	0,73	0,0198
1416259_at	Pex12	peroxisomal biogenesis factor 12	0,73	0,0267
1435594_at	Atl2	atlastin GTPase 2	0,73	0,0226
1423497_at	Klhl10	kelch-like 10 (Drosophila)	0,73	0,0446
1449194_at	Mrps25	mitochondrial ribosomal protein S25	0,73	0,0108
1416522_a_at	Grcc10	gene rich cluster, C10 gene	0,73	0,0012
1447701_x_at	Idh3a	isocitrate dehydrogenase 3 (NAD+) alpha	0,73	0,0259
1428743_at	Bri3bp	Bri3 binding protein	0,73	0,0088
1454827_at	Pogz	pogo transposable element with ZNF domain	0,73	0,0066
1421309_at	Mgmt	O-6-methylguanine-DNA methyltransferase	0,73	0,0145
1436038_a_at	Pigp	phosphatidylinositol glycan anchor biosynthesis, class P	0,73	0,0079
1441807_s_at	NA	NA	0,73	0,0497
1455941_s_at	Map2k5	mitogen-activated protein kinase kinase 5	0,73	0,0249
1424022_at	Osgin1	oxidative stress induced growth inhibitor 1	0,73	0,0414
1416999_at	Smpd2	sphingomyelin phosphodiesterase 2, neutral	0,73	0,0097
1418473_at	Cutc	cutC copper transporter homolog (E.coli)	0,73	0,0052
1448065_at	NA	NA	0,73	0,0155
1454532_at	C030043A13Rik	RIKEN cDNA C030043A13 gene	0,73	0,0385

1435074_at	Tmem106b	transmembrane protein 106B	0,73	0,0031
1416620_at	Smarcal1	SWI/SNF related matrix associated, actin dependent regulator of chromatin, subfamily a-like 1	0,73	0,0157
1429329_at	Cox10	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast)	0,73	0,0271
1428769_at	Tatdn3	TatD DNase domain containing 3	0,73	0,0044
1441919_x_at	Crat	carnitine acetyltransferase	0,73	0,0018
1418951_at	Txlnb	taxilin beta	0,73	0,0243
1423583_at	Fem1a	feminization 1 homolog a (C. elegans)	0,73	0,0209
1448913_at	Smarcd1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1	0,73	0,0178
1422581_at	Pias1	protein inhibitor of activated STAT 1	0,73	0,0033
1450606_at	Pnmt	phenylethanolamine-N-methyltransferase	0,73	0,0217
1433680_x_at	Siva1	SIVA1, apoptosis-inducing factor	0,73	0,0169
1430369_at	Epb4.1	erythrocyte protein band 4.1	0,73	0,0266
1438041_at	Pde7a	phosphodiesterase 7A	0,73	0,0194
1435127_a_at	Ormdl1	ORM1-like 1 (S. cerevisiae)	0,74	0,0009
1426561_a_at	Npnt	nephronectin	0,74	0,0232
1417690_at	Prkag1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	0,74	0,0094
1427114_at	Ttc19	tetratricopeptide repeat domain 19	0,74	0,0281
1416367_at	Fmc1	formation of mitochondrial complexes 1 homolog (S. cerevisiae)	0,74	0,0007
1436622_at	Iqsec2	IQ motif and Sec7 domain 2	0,74	0,0478
1420864_at	Zfp161	zinc finger protein 161	0,74	0,0346
1416373_at	Nfs1	nitrogen fixation gene 1 (S. cerevisiae)	0,74	0,0006
1444307_at	NA	NA	0,74	0,0027
1455204_at	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	0,74	0,0069
1455227_at	Aadacl1	arylacetamide deacetylase-like 1	0,74	0,0033
1430128_a_at	Reep6	receptor accessory protein 6	0,74	0,0260
1421861_at	Clstn1	calsyntenin 1	0,74	0,0146
1434417_at	Solh	small optic lobes homolog (Drosophila)	0,74	0,0304
1425628_a_at	Gtf2i	general transcription factor II I	0,74	0,0005
1454815_at	Sertad2	SERTA domain containing 2	0,74	0,0032
1424697_at	Dtwd1	DTW domain containing 1	0,74	0,0219
1454675_at	Thra	thyroid hormone receptor alpha	0,74	0,0267
1436548_at	1810012P15Rik	RIKEN cDNA 1810012P15 gene	0,74	0,0252
1416353_at	Nr1h2	nuclear receptor subfamily 1, group H, member 2	0,74	0,0119
1435333_at	1110007M04Rik	RIKEN cDNA 1110007M04 gene	0,74	0,0133
1438477_a_at	Mcee	methylmalonyl CoA epimerase	0,74	0,0349
1438348_x_at	Ccbl1	cysteine conjugate-beta lyase 1	0,74	0,0077
1454835_at	Epm2aip1	EPM2A (laforin) interacting protein 1	0,74	0,0353
1450576_a_at	Sf3a2	splicing factor 3a, subunit 2	0,74	0,0054
1441377_at	Kif6	kinesin family member 6	0,74	0,0184
1419702_at	Taf1a	TATA box binding protein (Tbp)-associated factor, RNA polymerase I, A	0,74	0,0492
1456143_at	Prkcbp1	protein kinase C binding protein 1	0,74	0,0007
1423785_at	Egln1	EGL nine homolog 1 (C. elegans)	0,74	0,0003
1425981_a_at	Rbl2	retinoblastoma-like 2	0,74	0,0114
1452791_at	Coq2	coenzyme Q2 homolog, prenyltransferase (yeast)	0,74	0,0007
1454654_at	Dirc2	disrupted in renal carcinoma 2 (human)	0,74	0,0114
1459637_at	NA	NA	0,74	0,0066
1439117_at	Clmn	calmin	0,74	0,0203
1427342_at	Fastkd1	FAST kinase domains 1	0,74	0,0067

1422501_s_at	Idh3a	isocitrate dehydrogenase 3 (NAD+) alpha	0,74	0,0321
1423889_at	EG434402	predicted gene, EG434402	0,74	0,0010
1428706_at	Cenpv	centromere protein V	0,74	0,0240
1424052_at	Thap4	THAP domain containing 4	0,74	0,0038
1457054_a_at	D130020L05Rik	RIKEN cDNA D130020L05 gene	0,74	0,0264
1426445_at	Ctage5	CTAGE family, member 5	0,74	0,0040
1419331_at	Cdh17	cadherin 17	0,74	0,0497
1426746_at	1810026J23Rik	RIKEN cDNA 1810026J23 gene	0,74	0,0053
1428954_at	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	0,74	0,0192
1443901_at	5830404H04Rik	RIKEN cDNA 5830404H04 gene	0,74	0,0403
1451465_at	Ubl7	ubiquitin-like 7 (bone marrow stromal cell-derived)	0,74	0,0233
1438188_x_at	Slc25a29	solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), member 29	0,74	0,0458
1451381_at	1810020D17Rik	RIKEN cDNA 1810020D17 gene	0,74	0,0013
1425940_a_at	Ssbp3	single-stranded DNA binding protein 3	0,74	0,0386
1438809_at	Atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	0,74	0,0482
1448546_at	Rassf3	Ras association (RalGDS/AF-6) domain family member 3	0,74	0,0264
1447818_x_at	Rhebl1	Ras homolog enriched in brain like 1	0,74	0,0158
1437382_at	Acvr2a	activin receptor IIA	0,74	0,0080
1452636_x_at	Gtpbp5	GTP binding protein 5	0,74	0,0264
1419821_s_at	Idh1	isocitrate dehydrogenase 1 (NADP+), soluble	0,74	0,0158
1424223_at	1700020C11Rik	RIKEN cDNA 1700020C11 gene	0,74	0,0077
1419489_at	Fam19a5	family with sequence similarity 19, member A5	0,74	0,0290
1434073_at	Gprasp2	G protein-coupled receptor associated sorting protein 2	0,74	0,0094
1437364_at	Coq3	coenzyme Q3 homolog, methyltransferase (yeast)	0,74	0,0287
1421340_at	Map3k5	mitogen-activated protein kinase kinase kinase 5	0,74	0,0262
1450737_at	Polr3k	polymerase (RNA) III (DNA directed) polypeptide K	0,74	0,0466
1451219_at	Ormdl1	ORM1-like 1 (S. cerevisiae)	0,74	0,0354
1439521_at	NA	NA	0,74	0,0069
1427982_s_at	Syne2	synaptic nuclear envelope 2	0,74	0,0199
1417016_at	Mapkapk5	MAP kinase-activated protein kinase 5	0,74	0,0172
1417438_at	Rdh14	retinol dehydrogenase 14 (all-trans and 9-cis)	0,74	0,0055
1417421_at	S100a1	S100 calcium binding protein A1	0,74	0,0213
1435769_at	Akap9	A kinase (PRKA) anchor protein (yotiao) 9	0,74	0,0187
1430896_s_at	Nudt7	nudix (nucleoside diphosphate linked moiety X)-type motif 7	0,74	0,0438
1422888_at	Rnf5	ring finger protein 5	0,74	0,0087
1451014_at	Ror1	receptor tyrosine kinase-like orphan receptor 1	0,74	0,0094
1430651_s_at	Zfp191	zinc finger protein 191	0,75	0,0275
1451592_at	P42pop	Myb protein P42POP	0,75	0,0296
1449626_s_at	Acbd4	acyl-Coenzyme A binding domain containing 4	0,75	0,0095
1416319_at	Adk	adenosine kinase	0,75	0,0037
1449614_s_at	AI314976	expressed sequence AI314976	0,75	0,0145
1434066_at	Gtf3c1	general transcription factor III C 1	0,75	0,0124
1423750_a_at	Sf1	splicing factor 1	0,75	0,0284
1450992_a_at	Meis1	Meis homeobox 1	0,75	0,0459
1421019_at	1700021F05Rik	RIKEN cDNA 1700021F05 gene	0,75	0,0022
1433669_at	Akap8	A kinase (PRKA) anchor protein 8	0,75	0,0015

1418017_at	Pum2	pumilio 2 (Drosophila)	0,75	0,0386
1445352_at	NA	NA	0,75	0,0211
1437281_x_at	Xab2	XPA binding protein 2	0,75	0,0075
1448418_s_at	Wdr23	WD repeat domain 23	0,75	0,0232
1453141_at	0610009L18Rik	RIKEN cDNA 0610009L18 gene	0,75	0,0180
1434210_s_at	Lrig1	leucine-rich repeats and immunoglobulin-like domains 1	0,75	0,0297
1452438_s_at	Taf4a	TAF4A RNA polymerase II, TATA box binding protein (TBP)-associated factor	0,75	0,0339
1434663_at	2410129H14Rik	RIKEN cDNA 2410129H14 gene	0,75	0,0213
1459337_at	Alg6	asparagine-linked glycosylation 6 homolog (yeast, alpha-1,3,-glucosyltransferase)	0,75	0,0179
1424404_at	0610040J01Rik	RIKEN cDNA 0610040J01 gene	0,75	0,0088
1434616_at	Slc38a10	solute carrier family 38, member 10	0,75	0,0345
1457872_at	NA	NA	0,75	0,0187
1444755_at	Mad1l1	mitotic arrest deficient 1-like 1	0,75	0,0149
1451169_at	Nomo1	nodal modulator 1	0,75	0,0081
1450614_x_at	Ifna5	interferon alpha 5	0,75	0,0106
1416616_s_at	Clpp	caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli)	0,75	0,0037
1439858_at	NA	NA	0,75	0,0336
1422397_a_at	Il15ra	interleukin 15 receptor, alpha chain	0,75	0,0265
1452976_a_at	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	0,75	0,0434
1423938_at	Llgl2	lethal giant larvae homolog 2 (Drosophila)	0,75	0,0468
AFFX-PyruCarbMur/L09192_MB_at	Pcx	pyruvate carboxylase	0,75	0,0393
1433932_x_at	C030046I01Rik	RIKEN cDNA C030046I01 gene	0,75	0,0077
1456531_x_at	Prpf19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	0,75	0,0085
1448692_at	Ubqln4	ubiquilin 4	0,75	0,0413
1421409_at	Msi1	Musashi homolog 1(Drosophila)	0,75	0,0366
1449234_at	Car15	carbonic anhydrase 15	0,75	0,0033
1417208_at	Amacr	alpha-methylacyl-CoA racemase	0,75	0,0116
1451671_at	Gorasp1	golgi reassembly stacking protein 1	0,75	0,0469
1455059_at	Helz	helicase with zinc finger domain	0,75	0,0172
1443952_at	NA	NA	0,75	0,0313
1449023_a_at	Ezh1	enhancer of zeste homolog 1 (Drosophila)	0,75	0,0082
1452105_a_at	Tsc2	tuberous sclerosis 2	0,75	0,0043
1460189_at	Wdr23	WD repeat domain 23	0,75	0,0254
1437704_at	2900024O10Rik	RIKEN cDNA 2900024O10 gene	0,75	0,0405
1424553_at	Hhatl	hedgehog acyltransferase-like	0,75	0,0165
1434161_at	Lin52	lin-52 homolog (C. elegans)	0,75	0,0348
1452942_at	Tmem65	transmembrane protein 65	0,75	0,0111
1425037_at	Fgd4	FYVE, RhoGEF and PH domain containing 4	0,75	0,0258
1450048_a_at	Idh2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	0,75	0,0173
1420524_a_at	Masp2	mannan-binding lectin serine peptidase 2	0,75	0,0094
1424418_at	Slc25a38	solute carrier family 25, member 38	0,75	0,0156
1420661_a_at	4933439F18Rik	RIKEN cDNA 4933439F18 gene	0,75	0,0114
1419384_at	Pick1	protein interacting with C kinase 1	0,75	0,0211
1431523_at	4930564K09Rik	RIKEN cDNA 4930564K09 gene	0,75	0,0090

1440856_at	Mapk8	mitogen-activated protein kinase 8	0,75	0,0046
1418040_at	Tmem186	transmembrane protein 186	0,75	0,0069
1421535_a_at	Pde4a	phosphodiesterase 4A, cAMP specific	0,75	0,0300
1451404_at	ORF19	open reading frame 19	0,75	0,0096
1439234_a_at	Tm2d2	TM2 domain containing 2	0,75	0,0355
1434754_at	Garnl4	GTPase activating RANGAP domain-like 4	0,75	0,0033
1455614_at	Nr1i3	nuclear receptor subfamily 1, group I, member 3	0,75	0,0213
1419994_s_at	D10Ertd641e	DNA segment, Chr 10, ERATO Doi 641, expressed	0,75	0,0272
1426654_at	Zc3hc1	zinc finger, C3HC type 1	0,75	0,0249
1426669_at	C530044N13Rik	RIKEN cDNA C530044N13 gene	0,75	0,0269
1434426_at	Ncapd3	non-SMC condensin II complex, subunit D3	0,75	0,0352
1430426_at	4930540M05Rik	RIKEN cDNA 4930540M05 gene	0,75	0,0278
1428134_at	Coq9	coenzyme Q9 homolog (yeast)	0,75	0,0018
1440262_at	AI414108	expressed sequence AI414108	0,75	0,0213
1421129_a_at	Atp2a3	ATPase, Ca++ transporting, ubiquitous	0,75	0,0112
1434155_a_at	2310061I04Rik	RIKEN cDNA 2310061I04 gene	0,75	0,0330
1424422_s_at	Lenep	lens epithelial protein	0,75	0,0376
1436083_at	Lrp3	low density lipoprotein receptor-related protein 3	0,75	0,0312
1448286_at	Hsd17b10	hydroxysteroid (17-beta) dehydrogenase 10	0,75	0,0095
1436453_at	BB144871	expressed sequence BB144871	0,75	0,0429
1438366_x_at	Clcn3	chloride channel 3	0,75	0,0117
1421127_at	Tmem42	transmembrane protein 42	0,75	0,0417
1427750_at	Igk-V1	immunoglobulin kappa chain variable 1 (V1)	0,75	0,0373
1421265_a_at	Rbm38	RNA binding motif protein 38	0,75	0,0162
1452745_at	Trappc9	trafficking protein particle complex 9	0,75	0,0325
1440605_at	Fscn2	fascin homolog 2, actin-bundling protein, retinal (Strongylocentrotus purpuratus)	0,76	0,0106
1436597_at	Ankhd1	ankyrin repeat and KH domain containing 1	0,76	0,0162
1460582_x_at	NA	NA	0,76	0,0091
1450266_at	Scn10a	sodium channel, voltage-gated, type X, alpha	0,76	0,0204
1441445_at	Per3	period homolog 3 (Drosophila)	0,76	0,0282
1440936_at	Serac1	serine active site containing 1	0,76	0,0158
1431198_x_at	9430038I01Rik	RIKEN cDNA 9430038I01 gene	0,76	0,0249
1454640_at	Chchd7	coiled-coil-helix-coiled-coil-helix domain containing 7	0,76	0,0019
1415690_at	Mrpl27	mitochondrial ribosomal protein L27	0,76	0,0008
1434715_at	1600014C10Rik	RIKEN cDNA 1600014C10 gene	0,76	0,0121
1447592_at	Dbh	dopamine beta hydroxylase	0,76	0,0233
1416275_at	Slc26a6	solute carrier family 26, member 6	0,76	0,0387
1428106_at	1300001I01Rik	RIKEN cDNA 1300001I01 gene	0,76	0,0457
1416427_at	Ccni	cyclin I	0,76	0,0303
1450670_at	Dbh	dopamine beta hydroxylase	0,76	0,0029
1452684_at	Akt1s1	AKT1 substrate 1 (proline-rich)	0,76	0,0451
1421873_s_at	Rab24	RAB24, member RAS oncogene family	0,76	0,0040
1456569_x_at	Gsn	gelsolin	0,76	0,0019
1452136_at	Slc5a9	solute carrier family 5 (sodium/glucose cotransporter), member 9	0,76	0,0213
1451542_at	Ssbp2	single-stranded DNA binding protein 2	0,76	0,0147
1419687_at	Macrod1	MACRO domain containing 1	0,76	0,0018
1424282_at	Pet112l	PET112-like (yeast)	0,76	0,0029
1421962_at	Dnajb5	DnaJ (Hsp40) homolog, subfamily B, member 5	0,76	0,0131

1457059_at	Zfp438	zinc finger protein 438	0,76	0,0311
1416934_at	Mtm1	X-linked myotubular myopathy gene 1	0,76	0,0242
1438924_x_at	Fibp	fibroblast growth factor (acidic) intracellular binding protein	0,76	0,0300
1425808_a_at	Myocd	myocardin	0,76	0,0450
1452116_s_at	Atf2	activating transcription factor 2	0,76	0,0038
1419757_at	Pitpnm2	phosphatidylinositol transfer protein, membrane-associated 2	0,76	0,0102
1423690_s_at	Gpsm1	G-protein signalling modulator 1 (AGS3-like, C. elegans)	0,76	0,0013
1448445_at	Acp6	acid phosphatase 6, lysophosphatidic	0,76	0,0052
1427226_at	Epn2	epsin 2	0,76	0,0294
1424276_at	Snx16	sorting nexin 16	0,76	0,0455
1437697_at	Rad23a	RAD23a homolog (S. cerevisiae)	0,76	0,0488
1417138_s_at	Polr2e	polymerase (RNA) II (DNA directed) polypeptide E	0,76	0,0389
1460548_a_at	Eral1	Era (G-protein)-like 1 (E. coli)	0,76	0,0054
1422975_at	Mme	membrane metallo endopeptidase	0,76	0,0341
1422383_at	NA	NA	0,76	0,0432
1455734_at	Crbn	cereblon	0,76	0,0226
1438452_at	Nebl	nebulette	0,76	0,0204
1451665_a_at	Ap4s1	adaptor-related protein complex AP-4, sigma 1	0,76	0,0031
1421583_at	Creb1	cAMP responsive element binding protein 1	0,76	0,0291
1427758_x_at	Igh-6	immunoglobulin heavy chain 6 (heavy chain of IgM)	0,76	0,0370
1444028_s_at	Dock9	dedicator of cytokinesis 9	0,76	0,0014
1418286_a_at	Efnb1	ephrin B1	0,76	0,0168
1457696_at	Rilp	Rab interacting lysosomal protein	0,76	0,0195
1427130_x_at	1700021K02Rik	RIKEN cDNA 1700021K02 gene	0,76	0,0078
1422001_at	Inhbc	inhibin beta-C	0,76	0,0320
1444502_at	Pet112l	PET112-like (yeast)	0,76	0,0158
1417161_at	Cdk2ap2	CDK2-associated protein 2	0,76	0,0015
1451222_at	Btf3l4	basic transcription factor 3-like 4	0,76	0,0129
1437410_at	Aldh2	aldehyde dehydrogenase 2, mitochondrial	0,76	0,0452
1456559_at	Emx2os	empty spiracles homolog 2 (Drosophila) opposite strand	0,76	0,0272
1435986_x_at	Pcp4l1	Purkinje cell protein 4-like 1	0,76	0,0152
1438479_at	Zfp213	zinc finger protein 213	0,76	0,0435
1422121_at	Oprd1	opioid receptor, delta 1	0,76	0,0288
1425833_a_at	Hpca	hippocalcin	0,76	0,0362
1457355_at	Pnpla8	patatin-like phospholipase domain containing 8	0,76	0,0137
1421556_at	Serpina3a	serine (or cysteine) peptidase inhibitor, clade A, member 3A	0,76	0,0070
1451274_at	Ogdh	oxoglutarate dehydrogenase (lipoamide)	0,76	0,0056
1421909_at	Tcf20	transcription factor 20	0,76	0,0437
1416930_at	Ly6d	lymphocyte antigen 6 complex, locus D	0,76	0,0366
1426961_at	Phf20	PHD finger protein 20	0,76	0,0149
1423659_a_at	Tbc1d17	TBC1 domain family, member 17	0,76	0,0270
1439232_at	NA	NA	0,76	0,0045
1452625_at	Kctd2	potassium channel tetramerisation domain containing 2	0,76	0,0296
1416842_at	Gstm5	glutathione S-transferase, mu 5	0,76	0,0187
1423999_at	Abl1	c-abl oncogene 1, receptor tyrosine kinase	0,76	0,0245
1428181_at	Etfb	electron transferring flavoprotein, beta polypeptide	0,76	0,0011
1457303_at	Anks3	ankyrin repeat and sterile alpha motif domain containing 3	0,76	0,0201
1450289_at	Foxd2	forkhead box D2	0,76	0,0187
1439830_at	Map3k5	mitogen-activated protein kinase kinase kinase 5	0,76	0,0020
1436599_at	NA	NA	0,76	0,0417
1438638_x_at	Fam116b	family with sequence similarity 116, member B	0,76	0,0168

1424280_at	Mospd1	motile sperm domain containing 1	0,76	0,0364
1440285_at	Ppp1r9a	protein phosphatase 1, regulatory (inhibitor) subunit 9A	0,76	0,0455
1460674_at	Paqr7	progestin and adipoQ receptor family member VII	0,76	0,0113
1450848_at	Dap3	death associated protein 3	0,76	0,0014
1418851_at	Trim39	tripartite motif-containing 39	0,76	0,0371
1458635_at	4832428D23Rik	RIKEN cDNA 4832428D23 gene	0,76	0,0238
1449365_at	S1pr5	sphingosine-1-phosphate receptor 5	0,76	0,0062
1424026_s_at	BC013529	cDNA sequence BC013529	0,77	0,0088
1427552_a_at	Gstz1	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	0,77	0,0220
1452821_at	Tial1	Tia1 cytotoxic granule-associated RNA binding protein-like 1	0,77	0,0425
1426843_at	Atg2a	ATG2 autophagy related 2 homolog A (S. cerevisiae)	0,77	0,0445
1417402_at	1190017O12Rik	RIKEN cDNA 1190017O12 gene	0,77	0,0016
1453317_a_at	Khdrbs3	KH domain containing, RNA binding, signal transduction associated 3	0,77	0,0466
1434565_at	Cgrrf1	cell growth regulator with ring finger domain 1	0,77	0,0339
1434604_at	Eif5b	eukaryotic translation initiation factor 5B	0,77	0,0447
1433343_at	4930448K20Rik	RIKEN cDNA 4930448K20 gene	0,77	0,0158
1460196_at	Cbr1	carbonyl reductase 1	0,77	0,0132
1450306_at	Zp1	zona pellucida glycoprotein 1	0,77	0,0152
1433179_at	Morn1	MORN repeat containing 1	0,77	0,0152
1417908_s_at	Ube2l3	ubiquitin-conjugating enzyme E2L 3	0,77	0,0327
1434168_at	Peo1	progressive external ophthalmoplegia 1 (human)	0,77	0,0026
1424064_at	Rab1b	RAB1B, member RAS oncogene family	0,77	0,0315
1450561_a_at	Surf1	surfeit gene 1	0,77	0,0036
1437371_at	Fam160a1	family with sequence similarity 160, member A1	0,77	0,0459
1435755_at	1110001A16Rik	RIKEN cDNA 1110001A16 gene	0,77	0,0101
1422719_s_at	Nup50	nucleoporin 50	0,77	0,0473
1438058_s_at	Ptov1	prostate tumor over expressed gene 1	0,77	0,0101
1452095_a_at	H47	histocompatibility 47	0,77	0,0049
1436428_at	Chrnb2	cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal)	0,77	0,0172
1455084_x_at	Shmt2	serine hydroxymethyltransferase 2 (mitochondrial)	0,77	0,0192
1416775_at	Atp5sl	ATP5S-like	0,77	0,0284
1450187_a_at	Galt	galactose-1-phosphate uridyl transferase	0,77	0,0428
1434792_at	2010320M18Rik	RIKEN cDNA 2010320M18 gene	0,77	0,0468
1424391_at	Nrd1	nardilysin, N-arginine dibasic convertase, NRD convertase 1	0,77	0,0058
1417516_at	Ddit3	DNA-damage inducible transcript 3	0,77	0,0292
1451450_at	2010011I20Rik	RIKEN cDNA 2010011I20 gene	0,77	0,0224
1457271_at	Gm131	gene model 131, (NCBI)	0,77	0,0117
1424219_at	Mrm1	mitochondrial rRNA methyltransferase 1 homolog (S. cerevisiae)	0,77	0,0415
1417907_at	Ube2l3	ubiquitin-conjugating enzyme E2L 3	0,77	0,0354
1433905_at	Akap7	A kinase (PRKA) anchor protein 7	0,77	0,0130
1423456_at	Bzw2	basic leucine zipper and W2 domains 2	0,77	0,0028
1460434_at	Fundc2	FUN14 domain containing 2	0,77	0,0045
1454976_at	Sod2	superoxide dismutase 2, mitochondrial	0,77	0,0417
1417877_at	Eepd1	endonuclease/exonuclease/phosphatase family domain containing 1	0,77	0,0451
1443833_at	NA	NA	0,77	0,0393

1423641_s_at	Cnot7	CCR4-NOT transcription complex, subunit 7	0,77	0,0291
1428520_at	1110032A13Rik	RIKEN cDNA 1110032A13 gene	0,77	0,0142
1417241_at	Amz2	archaelysin family metallopeptidase 2	0,77	0,0008
1423663_at	Flcn	folliculin	0,77	0,0312
1418657_at	Ino80b	INO80 complex subunit B	0,77	0,0105
1423733_a_at	Fiz1	Flt3 interacting zinc finger protein 1	0,77	0,0227
1422103_a_at	Stat5b	signal transducer and activator of transcription 5B	0,77	0,0069
1424288_at	Mepce	methylphosphate capping enzyme	0,77	0,0249
1455640_a_at	Txn2	thioredoxin 2	0,77	0,0021
1438685_at	Zmym6	zinc finger, MYM-type 6	0,77	0,0245
1418202_a_at	Wiz	widely-interspaced zinc finger motifs	0,77	0,0017
1451696_at	Zfp64	zinc finger protein 64	0,77	0,0260
1453232_at	Calr3	calreticulin 3	0,77	0,0447
1441826_x_at	NA	NA	0,77	0,0026
1453342_at	Cdc40	cell division cycle 40 homolog (yeast)	0,77	0,0015
1460337_at	Sh3kbp1	SH3-domain kinase binding protein 1	0,77	0,0178
1441711_at	ENSMUSG00000054421	predicted gene, ENSMUSG00000054421	0,77	0,0158
1418437_a_at	Mlx	MAX-like protein X	0,77	0,0199
1424021_at	Arl6ip6	ADP-ribosylation factor-like 6 interacting protein 6	0,77	0,0442
1452291_at	Arap2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	0,77	0,0384
1454506_at	8430432A02Rik	RIKEN cDNA 8430432A02 gene	0,77	0,0247
1442446_at	Zfp523	zinc finger protein 523	0,77	0,0487
1424180_a_at	Med24	mediator complex subunit 24	0,77	0,0252
1425178_s_at	Shmt1	serine hydroxymethyltransferase 1 (soluble)	0,77	0,0062
1438705_at	Cbfa2t3	core-binding factor, runt domain, alpha subunit 2, translocated to, 3 (human)	0,77	0,0284
1445141_at	Ikbkb	inhibitor of kappaB kinase beta	0,77	0,0303
1420219_at	Dnajc21	DnaJ (Hsp40) homolog, subfamily C, member 21	0,77	0,0158
1422467_at	Ppt1	palmitoyl-protein thioesterase 1	0,77	0,0037
1415986_at	Clcn4-2	chloride channel 4-2	0,77	0,0031
1449019_at	Akap1	A kinase (PRKA) anchor protein 1	0,77	0,0010
1433936_at	0610010E21Rik	RIKEN cDNA 0610010E21 gene	0,77	0,0447
1423320_at	Dnase1l2	deoxyribonuclease 1-like 2	0,77	0,0357
1436773_x_at	Marveld1	MARVEL (membrane-associating) domain containing 1	0,77	0,0081
1434154_at	Kctd13	potassium channel tetramerisation domain containing 13	0,77	0,0375
1440608_at	NA	NA	0,77	0,0447
1435085_at	NA	NA	0,77	0,0490
1453930_at	1110015M06Rik	RIKEN cDNA 1110015M06 gene	0,77	0,0104
1452517_at	Plekhh1	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1	0,77	0,0158
1452533_at	Ryr3	ryanodine receptor 3	0,77	0,0137
1434471_at	BC003331	cDNA sequence BC003331	0,77	0,0440
1436079_s_at	Vapb	vesicle-associated membrane protein, associated protein B and C	0,77	0,0154
1432772_at	1700081H04Rik	RIKEN cDNA 1700081H04 gene	0,77	0,0114
1448095_at	NA	NA	0,77	0,0348
1418508_a_at	Grb2	growth factor receptor bound protein 2	0,77	0,0388
1438011_at	Pcyt1a	phosphate cytidylyltransferase 1, choline, alpha isoform	0,77	0,0183
1421197_a_at	Acin1	apoptotic chromatin condensation inducer 1	0,77	0,0277

1417708_at	Syt3	synaptotagmin III	0,77	0,0178
1451803_a_at	Vegfb	vascular endothelial growth factor B	0,77	0,0046
1419244_a_at	Rab14	RAB14, member RAS oncogene family	0,77	0,0295
1452970_at	Zmym2	zinc finger, MYM-type 2	0,77	0,0482
1434870_at	2810004N23Rik	RIKEN cDNA 2810004N23 gene	0,77	0,0119
1426602_at	Araf	v-raf murine sarcoma 3611 viral oncogene homolog	0,78	0,0298
1428213_at	Nsmce4a	non-SMC element 4 homolog A (S. cerevisiae)	0,78	0,0122
1449441_a_at	Wbp1	WW domain binding protein 1	0,78	0,0088
1450832_at	Hoxc5	homeo box C5	0,78	0,0254
1416402_at	Abcb10	ATP-binding cassette, sub-family B (MDR/TAP), member 10	0,78	0,0061
1455226_at	Spnb1	spectrin beta 1	0,78	0,0267
1424467_at	Phldb1	pleckstrin homology-like domain, family B, member 1	0,78	0,0269
1422057_at	Nodal	nodal	0,78	0,0478
1425419_a_at	Raf1	v-raf-leukemia viral oncogene 1	0,78	0,0380
1452585_at	Mrps28	mitochondrial ribosomal protein S28	0,78	0,0069
1426679_at	Zfp706	zinc finger protein 706	0,78	0,0055
1446473_at	4732418C07Rik	RIKEN cDNA 4732418C07 gene	0,78	0,0408
1433036_at	4930564B12Rik	RIKEN cDNA 4930564B12 gene	0,78	0,0295
1452341_at	Echs1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	0,78	0,0099
1452872_at	Ank3	ankyrin 3, epithelial	0,78	0,0166
1428355_at	Osbp2	oxysterol binding protein 2	0,78	0,0221
1450160_at	Lif	leukemia inhibitory factor	0,78	0,0193
1426499_at	Sh3glb2	SH3-domain GRB2-like endophilin B2	0,78	0,0468
1419137_at	Shank3	SH3/ankyrin domain gene 3	0,78	0,0220
1418699_s_at	Fech	ferrochelatase	0,78	0,0254
1455588_at	Lyrm4	LYR motif containing 4	0,78	0,0076
1416570_s_at	Gfm1	G elongation factor, mitochondrial 1	0,78	0,0253
1427951_s_at	Ccdc28a	coiled-coil domain containing 28A	0,78	0,0333
1444156_at	9230112E08Rik	RIKEN cDNA 9230112E08 gene	0,78	0,0440
1459859_x_at	Chrac1	chromatin accessibility complex 1	0,78	0,0064
1450835_a_at	Gfra4	glial cell line derived neurotrophic factor family receptor alpha 4	0,78	0,0165
1449635_at	Prpf19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	0,78	0,0444
1425680_a_at	Btrc	beta-transducin repeat containing protein	0,78	0,0107
1457119_at	NA	NA	0,78	0,0362
1436193_at	Man1c1	mannosidase, alpha, class 1C, member 1	0,78	0,0174
1421446_at	Prkcc	protein kinase C, gamma	0,78	0,0458
1448027_at	Ncoa3	nuclear receptor coactivator 3	0,78	0,0482
1424836_a_at	Clasp2	CLIP associating protein 2	0,78	0,0138
1428744_s_at	Bri3bp	Bri3 binding protein	0,78	0,0082
1433673_at	E130309D14Rik	RIKEN cDNA E130309D14 gene	0,78	0,0284
1417456_at	Gnpat	glyceronephosphate O-acyltransferase	0,78	0,0275
1456954_at	Kcna6	potassium voltage-gated channel, shaker-related, subfamily, member 6	0,78	0,0088
1420679_a_at	Aig1	androgen-induced 1	0,78	0,0300
1417505_s_at	Il11ra1	interleukin 11 receptor, alpha chain 1	0,78	0,0030
1428775_at	1110008L16Rik	RIKEN cDNA 1110008L16 gene	0,78	0,0149
1419653_a_at	Ddx5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	0,78	0,0497

1437285_at	1110020G09Rik	RIKEN cDNA 1110020G09 gene	0,78	0,0471
1430525_at	2310001K24Rik	RIKEN cDNA 2310001K24 gene	0,78	0,0331
1417387_at	Med31	mediator of RNA polymerase II transcription, subunit 31 homolog (yeast)	0,78	0,0109
1440772_x_at	9530077C05Rik	RIKEN cDNA 9530077C05 gene	0,78	0,0298
1457391_at	Vamp3	vesicle-associated membrane protein 3	0,78	0,0170
1444949_at	NA	NA	0,78	0,0290
1427887_at	Rprd1b	regulation of nuclear pre-mRNA domain containing 1B	0,78	0,0073
1451354_at	Foxred1	FAD-dependent oxidoreductase domain containing 1	0,78	0,0312
1417283_at	Lynx1	Ly6/neurotoxin 1	0,78	0,0133
1426998_at	Zfand3	zinc finger, AN1-type domain 3	0,78	0,0192
1420113_s_at	2410022L05Rik	RIKEN cDNA 2410022L05 gene	0,78	0,0188
1438693_at	Tmem110	transmembrane protein 110	0,78	0,0455
1433950_at	Igsf21	immunoglobin superfamily, member 21	0,78	0,0151
1432589_at	NA	NA	0,78	0,0274
1451302_at	1110012L19Rik	RIKEN cDNA 1110012L19 gene	0,78	0,0161
1441949_x_at	Slc39a6	solute carrier family 39 (metal ion transporter), member 6	0,78	0,0466
1456077_x_at	Cdc25c	cell division cycle 25 homolog C (S. pombe)	0,78	0,0470
1426482_at	Prkrir	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)	0,78	0,0392
1432372_a_at	Spr	sepiapterin reductase	0,78	0,0173
1425177_at	Shmt1	serine hydroxymethyltransferase 1 (soluble)	0,78	0,0275
1417665_a_at	Cpsf1	cleavage and polyadenylation specific factor 1	0,78	0,0335
1428298_at	1700029G01Rik	RIKEN cDNA 1700029G01 gene	0,78	0,0306
1451935_a_at	Spint2	serine protease inhibitor, Kunitz type 2	0,78	0,0447
1452028_a_at	Cdh23	cadherin 23 (otocadherin)	0,78	0,0398
1442696_at	NA	NA	0,78	0,0096
1454731_at	Myo10	myosin X	0,78	0,0188
1451305_at	Cby1	chibby homolog 1 (Drosophila)	0,78	0,0216
1449893_a_at	Lrig1	leucine-rich repeats and immunoglobulin-like domains 1	0,78	0,0370
1431895_at	4933434M16Rik	RIKEN cDNA 4933434M16 gene	0,78	0,0437
1426586_at	Slc25a11	solute carrier family 25 (mitochondrial carrier oxoglutarate carrier), member 11	0,78	0,0251
1416012_at	Ehd1	EH-domain containing 1	0,78	0,0487
1416292_at	Prdx3	peroxiredoxin 3	0,78	0,0022
1440964_s_at	Cbfa2t3	core-binding factor, runt domain, alpha subunit 2, translocated to, 3 (human)	0,78	0,0098
1448670_at	Ube2e3	ubiquitin-conjugating enzyme E2E 3, UBC4/5 homolog (yeast)	0,78	0,0460
1451153_a_at	Cyhr1	cysteine and histidine rich 1	0,78	0,0133
1424345_s_at	Ube2m	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast)	0,78	0,0201
1428238_at	Orc3l	origin recognition complex, subunit 3-like (S. cerevisiae)	0,78	0,0363
1434900_at	Mkl1	MKL (megakaryoblastic leukemia)/myocardin-like 1	0,78	0,0243
1418529_at	Osgep	O-sialoglycoprotein endopeptidase	0,78	0,0069
1454773_at	Rxra	retinoid X receptor alpha	0,78	0,0286
1452660_s_at	Klhl7	kelch-like 7 (Drosophila)	0,78	0,0409
1423711_at	Ndufaf1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1	0,78	0,0259
1420848_at	Sufu	suppressor of fused homolog (Drosophila)	0,78	0,0102

1449396_at	Aoc3	amine oxidase, copper containing 3	0,78	0,0417
1460436_at	Ndst1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	0,78	0,0096
1426046_a_at	Rabggta	Rab geranylgeranyl transferase, a subunit	0,78	0,0102
1419786_at	Ltbp1	latent transforming growth factor beta binding protein 1	0,78	0,0495
1428428_at	Abhd11	abhydrolase domain containing 11	0,78	0,0035
1423990_at	Rab28	RAB28, member RAS oncogene family	0,78	0,0007
1420735_at	Gabrr2	gamma-aminobutyric acid (GABA-C) receptor, subunit rho 2	0,78	0,0378
1436366_at	Ppp1r15b	protein phosphatase 1, regulatory (inhibitor) subunit 15b	0,78	0,0219
1455139_at	AI851716	expressed sequence AI851716	0,78	0,0434
1459534_at	NA	NA	0,78	0,0436
1455450_at	Ptpn3	protein tyrosine phosphatase, non-receptor type 3	0,78	0,0159
1426490_at	Bfar	bifunctional apoptosis regulator	0,78	0,0279
1444127_at	Asb1	ankyrin repeat and SOCS box-containing 1	0,78	0,0374
1458514_at	AA536887	expressed sequence AA536887	0,78	0,0448
1422333_at	Cyp21a1	cytochrome P450, family 21, subfamily a, polypeptide 1	0,78	0,0493
1460687_at	Setd8	SET domain containing (lysine methyltransferase) 8	0,78	0,0424
1424153_s_at	Sall4	sal-like 4 (Drosophila)	0,78	0,0493
1450311_at	Slc8a3	solute carrier family 8 (sodium/calcium exchanger), member 3	0,78	0,0065
1434261_at	Sipa1l2	signal-induced proliferation-associated 1 like 2	0,78	0,0489
1436228_at	Ctbp2	C-terminal binding protein 2	0,78	0,0335
1457329_at	NA	NA	0,78	0,0302
1419839_x_at	Prpf19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	0,78	0,0465
1443306_at	NA	NA	0,78	0,0215
1422060_at	Parvb	parvin, beta	0,78	0,0080
1422069_at	Mc1r	melanocortin 1 receptor	0,79	0,0231
1452615_s_at	Trpt1	tRNA phosphotransferase 1	0,79	0,0348
1453113_at	Wdsub1	WD repeat, SAM and U-box domain containing 1	0,79	0,0023
1434633_at	Crebbp	CREB binding protein	0,79	0,0395
1418068_at	Ndufa10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	0,79	0,0033
1421533_at	Slc7a1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	0,79	0,0304
1453484_at	1700081D17Rik	RIKEN cDNA 1700081D17 gene	0,79	0,0324
1448630_a_at	Sdhc	succinate dehydrogenase complex, subunit C, integral membrane protein	0,79	0,0096
1454267_a_at	Prss32	protease, serine, 32	0,79	0,0227
1452053_a_at	Tmem33	transmembrane protein 33	0,79	0,0193
1433524_at	AU042671	expressed sequence AU042671	0,79	0,0302
1459772_at	Hps3	Hermansky-Pudlak syndrome 3 homolog (human)	0,79	0,0335
1432168_at	D730045A05Rik	RIKEN cDNA D730045A05 gene	0,79	0,0144
1433250_at	4931409D07Rik	RIKEN cDNA 4931409D07 gene	0,79	0,0207
1426689_s_at	Sdha	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	0,79	0,0192
1423305_at	Extl1	exostoses (multiple)-like 1	0,79	0,0061
1455777_x_at	Hsd17b4	hydroxysteroid (17-beta) dehydrogenase 4	0,79	0,0447
1416148_at	Laptm4b	lysosomal-associated protein transmembrane 4B	0,79	0,0339
1435443_at	Eya3	eyes absent 3 homolog (Drosophila)	0,79	0,0346
1416381_a_at	Prdx5	peroxiredoxin 5	0,79	0,0014
1449333_at	Sf3a1	splicing factor 3a, subunit 1	0,79	0,0282
1442783_x_at	NA	NA	0,79	0,0358

1439331_at	4932439E07Rik	RIKEN cDNA 4932439E07 gene	0,79	0,0345
1416988_at	Msh2	mutS homolog 2 (E. coli)	0,79	0,0264
1436358_at	Atpaf1	ATP synthase mitochondrial F1 complex assembly factor 1	0,79	0,0467
1424316_at	Slc25a19	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19	0,79	0,0158
1424025_at	BC013529	cDNA sequence BC013529	0,79	0,0042
1452797_at	Fastkd3	FAST kinase domains 3	0,79	0,0171
1448921_a_at	Mrps9	mitochondrial ribosomal protein S9	0,79	0,0111
1448321_at	Smoc1	SPARC related modular calcium binding 1	0,79	0,0404
1427680_a_at	Nfib	nuclear factor I/B	0,79	0,0163
1436067_at	Zbtb10	zinc finger and BTB domain containing 10	0,79	0,0309
1428716_at	Pex1	peroxisomal biogenesis factor 1	0,79	0,0192
1421901_at	Eif2ak1	eukaryotic translation initiation factor 2 alpha kinase 1	0,79	0,0240
1452782_a_at	Txn2	thioredoxin 2	0,79	0,0066
1433713_at	Gcn1l1	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	0,79	0,0246
1455918_at	Adrb3	adrenergic receptor, beta 3	0,79	0,0109
1435004_at	Pank4	pantothenate kinase 4	0,79	0,0356
1453663_at	4932442E05Rik	RIKEN cDNA 4932442E05 gene	0,79	0,0211
1438315_x_at	Akr7a5	aldo-keto reductase family 7, member A5 (aflatoxin aldehyde reductase)	0,79	0,0304
1438930_s_at	Mecp2	methyl CpG binding protein 2	0,79	0,0437
1418644_a_at	Stk11	serine/threonine kinase 11	0,79	0,0273
1436812_at	Fkrp	fukutin related protein	0,79	0,0272
1431904_at	4933427G17Rik	RIKEN cDNA 4933427G17 gene	0,79	0,0098
1433000_at	1700019L13Rik	RIKEN cDNA 1700019L13 gene	0,79	0,0455
1438563_s_at	Mrps24	mitochondrial ribosomal protein S24	0,79	0,0447
1455612_at	AI848218	expressed sequence AI848218	0,79	0,0479
1444472_at	NA	NA	0,79	0,0489
1460681_at	Ceacam2	carcinoembryonic antigen-related cell adhesion molecule 2	0,79	0,0176
1429248_at	2810002N01Rik	RIKEN cDNA 2810002N01 gene	0,79	0,0104
1433882_at	Cnot10	CCR4-NOT transcription complex, subunit 10	0,79	0,0412
1423913_at	Hectd3	HECT domain containing 3	0,79	0,0066
1453795_at	Fahd2a	fumarylacetoacetate hydrolase domain containing 2A	0,79	0,0038
1452506_a_at	Ilkap	integrin-linked kinase-associated serine/threonine phosphatase 2C	0,79	0,0415
1417275_at	Mal	myelin and lymphocyte protein, T-cell differentiation protein	0,79	0,0431
1449000_at	D10Jhu81e	DNA segment, Chr 10, Johns Hopkins University 81 expressed	0,79	0,0045
1451292_at	Zfp212	Zinc finger protein 212	0,79	0,0129
1421557_x_at	Txn2	thioredoxin 2	0,79	0,0026
1435149_at	Plcg1	phospholipase C, gamma 1	0,79	0,0052
1418331_at	1110031I02Rik	RIKEN cDNA 1110031I02 gene	0,79	0,0096
1428208_at	Bcl7a	B-cell CLL/lymphoma 7A	0,79	0,0330
1429598_at	2310042D19Rik	RIKEN cDNA 2310042D19 gene	0,79	0,0086
1429945_at	Klhl35	kelch-like 35 (Drosophila)	0,79	0,0103
1419071_at	Cys1	cystin 1	0,79	0,0234
1449786_at	Zdhhc7	zinc finger, DHHC domain containing 7	0,79	0,0429

1418034_at	Mrps9	mitochondrial ribosomal protein S9	0,79	0,0104
1444446_at	NA	NA	0,79	0,0176
1425543_s_at	Plekha5	pleckstrin homology domain containing, family A member 5	0,79	0,0069
1451747_a_at	Atg12	autophagy-related 12 (yeast)	0,79	0,0443
1456289_at	Hamp2	hepcidin antimicrobial peptide 2	0,79	0,0284
1451591_a_at	Efnb1	ephrin B1	0,79	0,0255
1419210_at	Hrh1	histamine receptor H1	0,79	0,0303
1439246_x_at	Tnrc6a	trinucleotide repeat containing 6a	0,79	0,0289
1416510_at	Mrpl4	mitochondrial ribosomal protein L4	0,79	0,0137
1453311_at	2310008B10Rik	RIKEN cDNA 2310008B10 gene	0,79	0,0466
1420641_a_at	Sqrdl	sulfide quinone reductase-like (yeast)	0,79	0,0297
1440467_at	4922501C03Rik	RIKEN cDNA 4922501C03 gene	0,79	0,0150
1418578_at	Dgka	diacylglycerol kinase, alpha	0,79	0,0407
1453271_at	Phf14	PHD finger protein 14	0,79	0,0061
1434984_at	Plk5	polo-like kinase 5 (Drosophila)	0,79	0,0144
1430494_at	2010005J08Rik	RIKEN cDNA 2010005J08 gene	0,79	0,0046
1441755_at	Mapk15	mitogen-activated protein kinase 15	0,79	0,0445
1426890_a_at	Rpap1	RNA polymerase II associated protein 1	0,79	0,0475
1423144_at	Pik3ca	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	0,79	0,0139
1418582_at	Cbfa2t3	core-binding factor, runt domain, alpha subunit 2, translocated to, 3 (human)	0,79	0,0197
1453587_at	Ggt6	gamma-glutamyltransferase 6	0,79	0,0295
1451106_at	Tut1	terminal uridylyl transferase 1, U6 snRNA-specific	0,79	0,0211
1454848_at	Ppp1r12c	protein phosphatase 1, regulatory (inhibitor) subunit 12C	0,79	0,0442
1431002_x_at	Fahd2a	fumarylacetoacetate hydrolase domain containing 2A	0,80	0,0293
1455042_at	NA	NA	0,80	0,0345
1442588_at	EG329217	predicted gene, EG329217	0,80	0,0164
1427959_at	Abhd10	abhydrolase domain containing 10	0,80	0,0374
1430116_at	Cyp4f41-ps	cytochrome P450, family 4, subfamily f, polypeptide 41 pseudogene	0,80	0,0267
1438416_at	Med16	mediator complex subunit 16	0,80	0,0187
1453086_at	6330408A02Rik	RIKEN cDNA 6330408A02 gene	0,80	0,0370
1438895_at	A430102J17Rik	RIKEN cDNA A430102J17 gene	0,80	0,0445
1419013_at	Gpatch1	G patch domain containing 1	0,80	0,0315
1433299_at	5830461L22Rik	RIKEN cDNA 5830461L22 gene	0,80	0,0498
1436201_x_at	Mbp	myelin basic protein	0,80	0,0303
1455198_a_at	Ppp2r3a	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha	0,80	0,0205
1440777_x_at	Ptgfr	prostaglandin F receptor	0,80	0,0187
1435464_at	1110003E01Rik	RIKEN cDNA 1110003E01 gene	0,80	0,0137
1418750_at	Plxnb3	plexin B3	0,80	0,0475
1416933_at	Por	P450 (cytochrome) oxidoreductase	0,80	0,0282
1428431_at	Zcchc24	zinc finger, CCHC domain containing 24	0,80	0,0217
1429953_at	2210011C24Rik	RIKEN cDNA 2210011C24 gene	0,80	0,0354
1435018_at	5930434B04Rik	RIKEN cDNA 5930434B04 gene	0,80	0,0213
1423146_at	Hes5	hairy and enhancer of split 5 (Drosophila)	0,80	0,0232
1424828_a_at	Fh1	fumarate hydratase 1	0,80	0,0023

1425132_at	Neto1	neuropilin (NRP) and tolloid (TLL)-like 1	0,80	0,0407
1432197_at	4933417D19Rik	RIKEN cDNA 4933417D19 gene	0,80	0,0241
1451448_a_at	1110005A03Rik	RIKEN cDNA 1110005A03 gene	0,80	0,0207
1421708_a_at	Stat6	signal transducer and activator of transcription 6	0,80	0,0474
1424628_a_at	Ndufv3	NADH dehydrogenase (ubiquinone) flavoprotein 3	0,80	0,0019
1454212_x_at	Gsdmcl2	gasdermin C-like 2	0,80	0,0178
1417182_at	Dnaja2	DnaJ (Hsp40) homolog, subfamily A, member 2	0,80	0,0231
1454873_at	Zfp775	zinc finger protein 775	0,80	0,0295
1424006_at	Aarsd1	alanyl-tRNA synthetase domain containing 1	0,80	0,0247
1447124_at	NA	NA	0,80	0,0381
1449845_a_at	Ephb4	Eph receptor B4	0,80	0,0290
1429054_at	Mrpl47	mitochondrial ribosomal protein L47	0,80	0,0386
1435499_at	Letm2	leucine zipper-EF-hand containing transmembrane protein 2	0,80	0,0433
1433441_at	Fbxl5	F-box and leucine-rich repeat protein 5	0,80	0,0386
1427091_at	Znfx1	zinc finger, NFX1-type containing 1	0,80	0,0459
1435949_at	Zc3h3	zinc finger CCCH type containing 3	0,80	0,0133
1429115_at	2010003O02Rik	RIKEN cDNA 2010003O02 gene	0,80	0,0380
1415987_at	Hdlbp	high density lipoprotein (HDL) binding protein	0,80	0,0321
1418183_a_at	Cyth1	cytohesin 1	0,80	0,0254
1454982_at	Arfgef2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	0,80	0,0061
1446803_at	NA	NA	0,80	0,0371
1449104_at	Upk3a	uroplakin 3A	0,80	0,0357
1448508_at	Traf3ip2	TRAF3 interacting protein 2	0,80	0,0236
1423285_at	Coch	coagulation factor C homolog (Limulus polyphemus)	0,80	0,0496
1438914_at	Ppp2r5a	protein phosphatase 2, regulatory subunit B (B56), alpha isoform	0,80	0,0293
1429663_at	Katnal2	katanin p60 subunit A-like 2	0,80	0,0324
1429351_at	Klhl24	kelch-like 24 (Drosophila)	0,80	0,0443
1419428_a_at	Gaa	glucosidase, alpha, acid	0,80	0,0435
1428723_at	2310047M10Rik	RIKEN cDNA 2310047M10 gene	0,80	0,0227
1452265_at	Clasp1	CLIP associating protein 1	0,80	0,0053
1427423_at	Cyb5rl	cytochrome b5 reductase-like	0,80	0,0174
1431721_a_at	Proz	protein Z, vitamin K-dependent plasma glycoprotein	0,80	0,0367
1447858_x_at	Il4ra	interleukin 4 receptor, alpha	0,80	0,0500
1433834_at	Mrz 06	membrane-associated ring finger (C3HC4) 6	0,80	0,0038
1425623_a_at	Cbs	cystathionine beta-synthase	0,80	0,0417
1444675_at	AL023051	expressed sequence AL023051	0,80	0,0302
1452591_a_at	Fam128b	family with sequence similarity 128, member B	0,80	0,0214
1452768_at	Tex261	testis expressed gene 261	0,80	0,0082
1439430_x_at	Fam83e	family with sequence similarity 83, member E	0,80	0,0368
1419484_a_at	Gbas	glioblastoma amplified sequence	0,80	0,0254
1447805_s_at	Slu7	SLU7 splicing factor homolog (S. cerevisiae)	0,80	0,0051
1417046_at	Tusc4	tumor suppressor candidate 4	0,80	0,0163
1423403_at	Mapkbp1	mitogen-activated protein kinase binding protein 1	0,80	0,0207
1452601_a_at	Acbd6	acyl-Coenzyme A binding domain containing 6	0,80	0,0243
1452017_at	Sox15	SRY-box containing gene 15	0,80	0,0173
1440182_at	Fzd10	frizzled homolog 10 (Drosophila)	0,80	0,0315
1427917_s_at	Ssbp3	single-stranded DNA binding protein 3	0,80	0,0055
1439834_at	2400009B08Rik	RIKEN cDNA 2400009B08 gene	0,80	0,0302
1418342_at	Rfc1	replication factor C (activator 1) 1	0,80	0,0324

1460682_s_at	Ceacam2	carcinoembryonic antigen-related cell adhesion molecule 2	0,80	0,0496
1435611_x_at	Ela3	elastase 3, pancreatic	0,80	0,0138
1424322_at	Apex2	apurinic/apyrimidinic endonuclease 2	0,80	0,0077
1443103_at	Gpr146	G protein-coupled receptor 146	0,80	0,0254
1436610_at	Ankrd12	ankyrin repeat domain 12	0,80	0,0178
1456164_at	AW011738	expressed sequence AW011738	0,80	0,0254
1425766_x_at	NA	NA	0,80	0,0132
1437192_x_at	Mt2	metallothionein 2	0,80	0,0130
1416789_at	Idh3g	isocitrate dehydrogenase 3 (NAD+), gamma	0,80	0,0054
1420950_at	Znrf1	zinc and ring finger 1	0,80	0,0399
1435762_at	Pacs1	phosphofurin acidic cluster sorting protein 1	0,80	0,0324
1455896_a_at	Kcnk1	potassium channel, subfamily K, member 1	0,80	0,0250
1421696_at	Pkhd1l1	polycystic kidney and hepatic disease 1-like 1	0,80	0,0312
1451307_at	Mrpl14	mitochondrial ribosomal protein L14	0,80	0,0453
1416127_a_at	Dnpep	aspartyl aminopeptidase	0,80	0,0226
1424108_at	Glo1	glyoxalase 1	0,80	0,0040
1423951_at	Tm2d3	TM2 domain containing 3	0,80	0,0126
1433624_at	Bat2l	HLA-B associated transcript 2-like	0,80	0,0068
1429907_at	1700094D03Rik	RIKEN cDNA 1700094D03 gene	0,80	0,0250
1439848_at	Bves	blood vessel epicardial substance	0,80	0,0357
1433647_s_at	Rhobtb3	Rho-related BTB domain containing 3	0,80	0,0420
1429862_at	Pla2g4e	phospholipase A2, group IVE	0,80	0,0417
1421681_at	Nrg4	neuregulin 4	0,80	0,0182
1435369_at	Fastkd5	FAST kinase domains 5	0,80	0,0417
1451961_a_at	Mbp	myelin basic protein	0,80	0,0200
1428108_x_at	Tmcc2	transmembrane and coiled-coil domains 2	0,80	0,0106
1458674_at	NA	NA	0,80	0,0426
1448811_at	Mrpl2	mitochondrial ribosomal protein L2	0,80	0,0048
1423582_at	Dmrt1	doublesex and mab-3 related transcription factor 1	0,80	0,0334
1448525_a_at	Bnip3l	BCL2/adenovirus E1B interacting protein 3-like	0,80	0,0241
1456759_at	NA	NA	0,80	0,0376
1422113_at	Slc5a5	solute carrier family 5 (sodium iodide symporter), member 5	0,80	0,0162
1416883_at	Clptm1	cleft lip and palate associated transmembrane protein 1	0,80	0,0196
1451754_a_at	Wdr45	WD repeat domain 45	0,80	0,0220
1434465_x_at	Vldlr	very low density lipoprotein receptor	0,81	0,0413
1425800_at	Rad9b	RAD9 homolog B (S. cerevisiae)	0,81	0,0371
1417000_at	Abtb1	ankyrin repeat and BTB (POZ) domain containing 1	0,81	0,0043
1451609_at	Tspan33	tetraspanin 33	0,81	0,0466
1452714_at	Tanc1	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	0,81	0,0305
1433586_at	Rgmb	RGM domain family, member B	0,81	0,0329
1435995_at	Mrpl22	mitochondrial ribosomal protein L22	0,81	0,0040
1449536_at	Kcnn1	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1	0,81	0,0445
1437037_x_at	Snd1	staphylococcal nuclease and tudor domain containing 1	0,81	0,0153
1428494_a_at	Polr2i	polymerase (RNA) II (DNA directed) polypeptide I	0,81	0,0146
1428588_a_at	Mrpl41	mitochondrial ribosomal protein L41	0,81	0,0348
1443961_at	AU017962	expressed sequence AU017962	0,81	0,0441
1426049_a_at	Terf2ip	telomeric repeat binding factor 2, interacting protein	0,81	0,0443
1456087_at	Nfia	nuclear factor I/A	0,81	0,0095
1454857_at	Rnf122	ring finger protein 122	0,81	0,0158
1448247_at	Bcl7b	B-cell CLL/lymphoma 7B	0,81	0,0048

1423107_at	Ube2b	ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae)	0,81	0,0256
1439289_s_at	Pnmal1	PNMA-like 1	0,81	0,0401
1457315_at	A230051G13Rik	RIKEN cDNA A230051G13 gene	0,81	0,0197
1455212_at	Wdr24	WD repeat domain 24	0,81	0,0061
1428207_at	Bcl7a	B-cell CLL/lymphoma 7A	0,81	0,0169
1427392_at	Dscaml1	Down syndrome cell adhesion molecule-like 1	0,81	0,0492
1426760_at	Ipo8	importin 8	0,81	0,0112
1460644_at	Bckdk	branched chain ketoacid dehydrogenase kinase	0,81	0,0300
1427282_a_at	Fxn	frataxin	0,81	0,0470
1432257_at	Gsdmcl1	gasdermin C-like 1	0,81	0,0181
1449113_at	Gpbp1l1	GC-rich promoter binding protein 1-like 1	0,81	0,0192
1436939_at	Unc45b	unc-45 homolog B (C. elegans)	0,81	0,0061
1433128_at	4930423C22Rik	RIKEN cDNA 4930423C22 gene	0,81	0,0359
1452795_at	Fcf1	FCF1 small subunit (SSU) processome component homolog (S. cerevisiae)	0,81	0,0383
1423712_a_at	Qars	glutaminyl-tRNA synthetase	0,81	0,0399
1432731_at	5830437K03Rik	RIKEN cDNA 5830437K03 gene	0,81	0,0137
1458767_at	NA	NA	0,81	0,0377
1449099_at	Lrba	LPS-responsive beige-like anchor	0,81	0,0219
1449302_at	Abca2	ATP-binding cassette, sub-family A (ABC1), member 2	0,81	0,0424
1423163_at	Bat4	HLA-B associated transcript 4	0,81	0,0275
1438144_x_at	Atxn2	ataxin 2	0,81	0,0158
1424184_at	Acadvl	acyl-Coenzyme A dehydrogenase, very long chain	0,81	0,0479
1434421_at	Islr2	immunoglobulin superfamily containing leucine-rich repeat 2	0,81	0,0440
1450943_at	Magohb	mago-nashi homolog B (Drosophila)	0,81	0,0377
1422394_at	NA	NA	0,81	0,0359
1415992_at	Pigo	phosphatidylinositol glycan anchor biosynthesis, class O	0,81	0,0151
1430945_at	A930028C08Rik	RIKEN cDNA A930028C08 gene	0,81	0,0201
1432060_at	Iqca	IQ motif containing with AAA domain	0,81	0,0284
1423908_at	Ndufs8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	0,81	0,0111
1440769_at	2010305A19Rik	RIKEN cDNA 2010305A19 gene	0,81	0,0338
1444884_at	Ppt1	palmitoyl-protein thioesterase 1	0,81	0,0293
1418754_at	Adcy8	adenylate cyclase 8	0,81	0,0442
1442238_a_at	Kif6	kinesin family member 6	0,81	0,0346
1418610_at	Slc17a6	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6	0,81	0,0478
1419547_at	Fahd1	fumarylacetoacetate hydrolase domain containing 1	0,81	0,0366
1444115_at	NA	NA	0,81	0,0407
1417737_at	Mrps31	mitochondrial ribosomal protein S31	0,81	0,0254
1451059_at	Zfp474	zinc finger protein 474	0,81	0,0207
1426708_at	Antxr2	anthrax toxin receptor 2	0,81	0,0267
1417551_at	Cln3	ceroid lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	0,81	0,0318
1459271_at	NA	NA	0,81	0,0314
1458393_at	Srr	serine racemase	0,81	0,0321
1431354_a_at	Fars2	phenylalanine-tRNA synthetase 2 (mitochondrial)	0,81	0,0177
1429539_at	Bcl2l13	BCL2-like 13 (apoptosis facilitator)	0,81	0,0329
1440323_at	Syt2	synaptotagmin II	0,81	0,0437
1418956_at	Tssk6	testis-specific serine kinase 6	0,81	0,0335
1441738_at	NA	NA	0,81	0,0088

1448432_at	Plcd1	phospholipase C, delta 1	0,81	0,0195
1431190_x_at	Fahd2a	fumarylacetoacetate hydrolase domain containing 2A	0,81	0,0074
1438289_a_at	Sumo1	SMT3 suppressor of mif two 3 homolog 1 (yeast)	0,81	0,0470
1450895_a_at	1810020G14Rik	RIKEN cDNA 1810020G14 gene	0,81	0,0070
1436814_at	NA	NA	0,81	0,0348
1429312_s_at	Ror1	receptor tyrosine kinase-like orphan receptor 1	0,81	0,0240
1417142_at	Fam120b	family with sequence similarity 120, member B	0,81	0,0312
1427790_at	Adam1a	a disintegrin and metallopeptidase domain 1a	0,81	0,0146
1442982_at	Ccdc66	coiled-coil domain containing 66	0,81	0,0346
1459660_at	NA	NA	0,81	0,0061
1415714_a_at	Snrnp27	small nuclear ribonucleoprotein 27 (U4/U6.U5)	0,81	0,0270
1435586_at	Pcid2	PCI domain containing 2	0,81	0,0173
1453390_at	4930428F12Rik	RIKEN cDNA 4930428F12 gene	0,81	0,0179
1424273_at	Cyp2c70	cytochrome P450, family 2, subfamily c, polypeptide 70	0,81	0,0442
1417118_a_at	Ard1a	ARD1 homolog A, N-acetyltransferase (S. cerevisiae)	0,81	0,0280
1427509_at	Baiap3	BAI1-associated protein 3	0,81	0,0175
1423780_at	Hibadh	3-hydroxyisobutyrate dehydrogenase	0,82	0,0295
1455018_at	Lmtk2	lemur tyrosine kinase 2	0,82	0,0260
1459848_x_at	Dbh	dopamine beta hydroxylase	0,82	0,0435
1426902_at	Coq6	coenzyme Q6 homolog (yeast)	0,82	0,0048
1459300_at	NA	NA	0,82	0,0272
1455958_s_at	Pptc7	PTC7 protein phosphatase homolog (S. cerevisiae)	0,82	0,0040
1438409_at	Cep63	centrosomal protein 63	0,82	0,0147
1445677_x_at	Slc35f2	solute carrier family 35, member F2	0,82	0,0340
1419713_at	Atp8b3	ATPase, class I, type 8B, member 3	0,82	0,0296
1446093_at	NA	NA	0,82	0,0205
1450340_a_at	Clcnkb	chloride channel Kb	0,82	0,0302
1424645_at	Tnrc6c	trinucleotide repeat containing 6C	0,82	0,0420
1452835_a_at	Polrmt	polymerase (RNA) mitochondrial (DNA directed)	0,82	0,0209
1452216_at	Mcat	malonyl CoA:ACP acyltransferase (mitochondrial)	0,82	0,0257
1423803_s_at	Gltscr2	glioma tumor suppressor candidate region gene 2	0,82	0,0296
1427565_a_at	Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	0,82	0,0293
1455684_at	Map3k9	mitogen-activated protein kinase kinase kinase 9	0,82	0,0326
1416657_at	Akt1	thymoma viral proto-oncogene 1	0,82	0,0449
1419575_s_at	Zfp292	zinc finger protein 292	0,82	0,0468
1451254_at	Ikbkap	inhibitor of kappa light polypeptide enhancer in B-cells, kinase complex-associated protein	0,82	0,0271
1415928_a_at	Map1lc3b	microtubule-associated protein 1 light chain 3 beta	0,82	0,0088
1447990_at	C76332	expressed sequence C76332	0,82	0,0174
1417977_at	Eif4e3	eukaryotic translation initiation factor 4E member 3	0,82	0,0069
1443849_x_at	Urod	uroporphyrinogen decarboxylase	0,82	0,0411
1416207_at	Taz	tafazzin	0,82	0,0276
1439222_at	Morc2b	microrchidia 2B	0,82	0,0452
1428862_at	Ttc17	tetratricopeptide repeat domain 17	0,82	0,0357
1454020_at	4930554H23Rik	RIKEN cDNA 4930554H23 gene	0,82	0,0235
1417535_at	Fbxo25	F-box protein 25	0,82	0,0061
1428898_at	Mon1a	MON1 homolog A (yeast)	0,82	0,0198
1427928_s_at	Pigu	phosphatidylinositol glycan anchor biosynthesis, class U	0,82	0,0227
1417619_at	Gadd45gip1	growth arrest and DNA-damage-inducible, gamma interacting protein 1	0,82	0,0169
1427939_s_at	Mycbp	c-myc binding protein	0,82	0,0295
1459029_at	Pak1	p21 (CDKN1A)-activated kinase 1	0,82	0,0450

1421903_at	Med29	mediator complex subunit 29	0,82	0,0440
1448563_at	Phb	prohibitin	0,82	0,0145
1446849_at	NA	NA	0,82	0,0275
1430879_at	C030008P14Rik	RIKEN cDNA C030008P14 gene	0,82	0,0199
1432823_at	Sypl2	synaptophysin-like 2	0,82	0,0199
1437779_at	Foxh1	forkhead box H1	0,82	0,0424
1451252_at	Irf2bp1	interferon regulatory factor 2 binding protein 1	0,82	0,0493
1448690_at	Kcnk1	potassium channel, subfamily K, member 1	0,82	0,0430
1421168_at	Abcg3	ATP-binding cassette, sub-family G (WHITE), member 3	0,82	0,0245
1427955_a_at	Deb1	differentially expressed in B16F10 1	0,82	0,0105
1433319_at	Sh3bgr	SH3-binding domain glutamic acid-rich protein	0,82	0,0446
1452425_at	Tnfrsf14	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)	0,82	0,0378
1432099_a_at	Prodh2	proline dehydrogenase (oxidase) 2	0,82	0,0466
1453363_at	Cacng2	calcium channel, voltage-dependent, gamma subunit 2	0,82	0,0489
1415685_at	Mtif2	mitochondrial translational initiation factor 2	0,82	0,0442
1424676_s_at	Sec14l4	SEC14-like 4 (S. cerevisiae)	0,82	0,0365
1460697_s_at	Snrnp27	small nuclear ribonucleoprotein 27 (U4/U6.U5)	0,82	0,0453
1451121_a_at	Gltscr2	glioma tumor suppressor candidate region gene 2	0,82	0,0336
1460194_at	Phyh	phytanoyl-CoA hydroxylase	0,82	0,0114
1455131_at	Opa3	optic atrophy 3 (human)	0,82	0,0370
1422566_at	Tcfeb	transcription factor EB	0,82	0,0137
1454657_s_at	Mak10	MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)	0,82	0,0184
1428448_a_at	Gtf3c2	general transcription factor IIIC, polypeptide 2, beta	0,82	0,0401
1424120_at	Rnf8	ring finger protein 8	0,82	0,0181
1458989_at	NA	NA	0,82	0,0296
1433286_at	4833417J16Rik	RIKEN cDNA 4833417J16 gene	0,82	0,0133
1438759_x_at	Adi1	acireductone dioxygenase 1	0,82	0,0179
1418332_a_at	Agtpbp1	ATP/GTP binding protein 1	0,82	0,0414
1424595_at	F11r	F11 receptor	0,82	0,0306
1417002_at	0610012G03Rik	RIKEN cDNA 0610012G03 gene	0,82	0,0084
1449129_a_at	Kcnip3	Kv channel interacting protein 3, calsenilin	0,82	0,0394
1417683_at	Diablo	diablo homolog (Drosophila)	0,82	0,0058
1423907_a_at	Ndufs8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	0,82	0,0087
1453197_at	Med25	mediator of RNA polymerase II transcription, subunit 25 homolog (yeast)	0,82	0,0417
1460545_at	Thrap3	thyroid hormone receptor associated protein 3	0,82	0,0265
1457387_at	Repin1	replication initiator 1	0,82	0,0442
1425143_a_at	Ndufs1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	0,82	0,0197
1424040_at	Mtap7d1	microtubule-associated protein 7 domain containing 1	0,82	0,0429
1452637_a_at	Bola1	bolA-like 1 (E. coli)	0,82	0,0162
1439921_at	100041660	predicted gene, 100041660	0,82	0,0258
1460529_at	4930455M05Rik	RIKEN cDNA 4930455M05 gene	0,82	0,0199
1443944_at	C530005A16Rik	RIKEN cDNA C530005A16 gene	0,82	0,0152
1457171_at	NA	NA	0,82	0,0443
1428411_at	1700020I14Rik	RIKEN cDNA 1700020I14 gene	0,82	0,0264
1421743_a_at	Pcbp2	poly(rC) binding protein 2	0,82	0,0442
1427125_s_at	Lrrc41	leucine rich repeat containing 41	0,83	0,0100
1451102_at	Cnot8	CCR4-NOT transcription complex, subunit 8	0,83	0,0120

1436137_at	Slc6a17	solute carrier family 6 (neurotransmitter transporter), member 17	0,83	0,0379
1435259_s_at	Tmem141	transmembrane protein 141	0,83	0,0225
1423972_at	Etfa	electron transferring flavoprotein, alpha polypeptide	0,83	0,0078
1448277_at	Pold2	polymerase (DNA directed), delta 2, regulatory subunit	0,83	0,0371
1437379_x_at	Trap1	TNF receptor-associated protein 1	0,83	0,0302
1449864_at	Il4	interleukin 4	0,83	0,0098
1429170_a_at	Mtf1	metal response element binding transcription factor 1	0,83	0,0302
1426583_at	Atf2	activating transcription factor 2	0,83	0,0203
1448046_at	Rabepk	Rab9 effector protein with kelch motifs	0,83	0,0389
1416763_at	Cdc123	cell division cycle 123 homolog (S. cerevisiae)	0,83	0,0377
1453994_at	C230094A16Rik	RIKEN cDNA C230094A16 gene	0,83	0,0327
1416210_at	Imp3	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)	0,83	0,0180
1425150_at	Acnat2	acyl-coenzyme A amino acid N-acyltransferase 2	0,83	0,0475
1426761_at	Aof2	amine oxidase (flavin containing) domain 2	0,83	0,0168
1437133_x_at	Akr1b3	aldo-keto reductase family 1, member B3 (aldose reductase)	0,83	0,0493
1416393_at	Emg1	EMG1 nucleolar protein homolog (S. cerevisiae)	0,83	0,0427
1432184_a_at	2610204M08Rik	RIKEN cDNA 2610204M08 gene	0,83	0,0375
1423883_at	Acsl1	acyl-CoA synthetase long-chain family member 1	0,83	0,0224
1449775_x_at	Slc35a4	solute carrier family 35, member A4	0,83	0,0300
1424036_at	Prpf6	PRP6 pre-mRNA splicing factor 6 homolog (yeast)	0,83	0,0283
1417950_a_at	Apoa2	apolipoprotein A-II	0,83	0,0330
1452934_at	Tmc5	transmembrane channel-like gene family 5	0,83	0,0370
1443210_at	ENSMUSG00000058736	predicted gene, ENSMUSG00000058736	0,83	0,0224
1416924_at	Bri3	brain protein I3	0,83	0,0114
1438191_a_at	Rnf40	ring finger protein 40	0,83	0,0150
1441600_at	C920021A13	hypothetical protein C920021A13	0,83	0,0443
1421585_at	Ccdc103	coiled-coil domain containing 103	0,83	0,0103
1416819_at	Cdc37	cell division cycle 37 homolog (S. cerevisiae)	0,83	0,0499
1436705_at	Mmgt1	membrane magnesium transporter 1	0,83	0,0142
1459113_at	NA	NA	0,83	0,0442
1449438_at	Dpm1	dolichol-phosphate (beta-D) mannosyltransferase 1	0,83	0,0461
1429547_at	4930578I06Rik	RIKEN cDNA 4930578I06 gene	0,83	0,0436
1434131_at	Rufy1	RUN and FYVE domain containing 1	0,83	0,0296
1455861_at	Epb4.1l5	erythrocyte protein band 4.1-like 5	0,83	0,0403
1448975_s_at	Ren1	renin 1 structural	0,83	0,0145
1426522_at	Hadhb	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	0,83	0,0464
1424878_at	Lrch4	leucine-rich repeats and calponin homology (CH) domain containing 4	0,83	0,0354
1417080_a_at	Ecsit	ECSIT homolog (Drosophila)	0,83	0,0073
1421262_at	Lipg	lipase, endothelial	0,83	0,0142
1435258_at	Tmem141	transmembrane protein 141	0,83	0,0495
1417286_at	Ndufa5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5	0,83	0,0130
1422453_at	Prpf8	pre-mRNA processing factor 8	0,83	0,0387
1459487_at	NA	NA	0,83	0,0393
1454759_at	Git1	G protein-coupled receptor kinase-interactor 1	0,83	0,0302

1451005_at	Sumo1	SMT3 suppressor of mif two 3 homolog 1 (yeast)	0,83	0,0449
1424541_at	Tmem70	transmembrane protein 70	0,83	0,0132
1451402_at	Ecd	ecdysoneless homolog (Drosophila)	0,83	0,0266
1450367_at	NA	NA	0,83	0,0442
1418266_at	Alox12b	arachidonate 12-lipoxygenase, 12R type	0,83	0,0384
1428000_at	Tmem60	transmembrane protein 60	0,83	0,0254
1452285_a_at	Eif3f	eukaryotic translation initiation factor 3, subunit F	0,83	0,0240
1428158_at	Akt1s1	AKT1 substrate 1 (proline-rich)	0,83	0,0240
1439278_at	Zbtb20	zinc finger and BTB domain containing 20	0,83	0,0264
1444002_at	Foxl2	forkhead box L2	0,83	0,0472
1437018_at	Pnma2	paraneoplastic antigen MA2	0,83	0,0420
1428464_at	Ndufa3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3	0,83	0,0067
1421347_at	Ftmt	ferritin mitochondrial	0,83	0,0245
1431891_at	Zswim5	zinc finger, SWIM domain containing 5	0,83	0,0200
1459260_at	NA	NA	0,83	0,0371
1425211_at	Gatc	glutamyl-tRNA(Gln) amidotransferase, subunit C homolog (bacterial)	0,83	0,0391
1447321_at	NA	NA	0,84	0,0466
1449623_at	Txnrd3	thioredoxin reductase 3	0,84	0,0459
1455283_x_at	Ndufs8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	0,84	0,0144
1460617_s_at	Rab6b	RAB6B, member RAS oncogene family	0,84	0,0430
1421014_a_at	Clybl	citrate lyase beta like	0,84	0,0295
1454438_at	Rab27a	RAB27A, member RAS oncogene family	0,84	0,0412
1460095_at	1110030E23Rik	RIKEN cDNA 1110030E23 gene	0,84	0,0483
1437629_at	Arhgef19	Rho guanine nucleotide exchange factor (GEF) 19	0,84	0,0428
1443638_at	NA	NA	0,84	0,0395
1445576_at	Rsph10b2	radial spoke head 10 homolog B (Chlamydomonas)	0,84	0,0287
1418127_a_at	Aifm1	apoptosis-inducing factor, mitochondrion-associated 1	0,84	0,0497
1441439_at	Ucn3	urocortin 3	0,84	0,0485
1434656_at	B230339M05Rik	RIKEN cDNA B230339M05 gene	0,84	0,0493
1450490_at	Kcna7	potassium voltage-gated channel, shaker-related subfamily, member 7	0,84	0,0398
1434344_at	Gpkow	G patch domain and KOW motifs	0,84	0,0493
1453731_a_at	Tmem77	transmembrane protein 77	0,84	0,0406
1444837_at	NA	NA	0,84	0,0478
1449108_at	Fdx1	ferredoxin 1	0,84	0,0222
1438206_a_at	Sys1	SYS1 Golgi-localized integral membrane protein homolog (S. cerevisiae)	0,84	0,0393
1451282_at	Arap3	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3	0,84	0,0321
1440024_at	NA	NA	0,84	0,0483
1428495_at	2410003K15Rik	RIKEN cDNA 2410003K15 gene	0,84	0,0298
1448237_x_at	Ldhb	lactate dehydrogenase B	0,84	0,0076
1422066_x_at	Klrb1b	killer cell lectin-like receptor subfamily B member 1B	0,84	0,0264
1424888_at	37316	membrane-associated ring finger (C3HC4) 2	0,84	0,0487
1433773_at	Rrm2b	ribonucleotide reductase M2 B (TP53 inducible)	0,84	0,0345
1436419_a_at	1700097N02Rik	RIKEN cDNA 1700097N02 gene	0,84	0,0329
1417720_at	Polr2j	polymerase (RNA) II (DNA directed) polypeptide J	0,84	0,0102
1458494_at	NA	NA	0,84	0,0381
1428589_at	Mrpl41	mitochondrial ribosomal protein L41	0,84	0,0113
1427422_at	EG624219	predicted gene, EG624219	0,84	0,0477
1416709_a_at	Ngrn	neugrin, neurite outgrowth associated	0,84	0,0192

1417193_at	Sod2	superoxide dismutase 2, mitochondrial	0,84	0,0056
1457624_at	Rab8a	RAB8A, member RAS oncogene family	0,84	0,0239
1434179_at	Mll3	myeloid/lymphoid or mixed-lineage leukemia 3	0,84	0,0478
1454432_at	4933423N03Rik	RIKEN cDNA 4933423N03 gene	0,84	0,0449
1447281_at	100042277	predicted gene, 100042277	0,84	0,0425
1417098_s_at	Mecr	mitochondrial trans-2-enoyl-CoA reductase	0,84	0,0321
1426517_at	Gnaz	guanine nucleotide binding protein, alpha z subunit	0,84	0,0468
1439280_at	OTTMUSG00000010464	predicted gene, OTTMUSG00000010464	0,84	0,0227
1415736_at	Pfdn5	prefoldin 5	0,84	0,0255
1431495_at	6030440G07Rik	RIKEN cDNA 6030440G07 gene	0,84	0,0485
1434387_at	Itfg3	integrin alpha FG-GAP repeat containing 3	0,84	0,0206
1418709_at	Cox7a1	cytochrome c oxidase, subunit VIIa 1	0,84	0,0085
1426247_at	Stk24	serine/threonine kinase 24 (STE20 homolog, yeast)	0,84	0,0477
1448003_at	1810043H04Rik	RIKEN cDNA 1810043H04 gene	0,84	0,0374
1422897_at	Slc22a12	solute carrier family 22 (organic anion/cation transporter), member 12	0,84	0,0173
1424554_at	Ppp1r8	protein phosphatase 1, regulatory (inhibitor) subunit 8	0,84	0,0412
1418988_at	Pex7	peroxisomal biogenesis factor 7	0,84	0,0325
1430211_at	4930415O20Rik	RIKEN cDNA 4930415O20 gene	0,84	0,0181
1416722_at	Hmg20a	high mobility group 20A	0,84	0,0256
1422321_a_at	Sf1	splicing factor 1	0,84	0,0243
1427587_at	Zfp28	zinc finger protein 28	0,84	0,0336
1423492_at	Mrpl45	mitochondrial ribosomal protein L45	0,84	0,0470
1446119_at	NA	NA	0,84	0,0405
1417459_at	Dcpp1	demilune cell and parotid protein 1	0,84	0,0435
1452266_at	Las1l	LAS1-like (S. cerevisiae)	0,84	0,0402
1426019_at	Plaa	phospholipase A2, activating protein	0,84	0,0362
1450452_a_at	Narfl	nuclear prelamin A recognition factor-like	0,84	0,0447
1448427_at	Ndufa6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	0,84	0,0111
1449253_at	Smc1b	structural maintenance of chromosomes 1B	0,84	0,0478
1428345_at	Ppapdc2	phosphatidic acid phosphatase type 2 domain containing 2	0,84	0,0314
1459868_x_at	100038993	predicted gene, 100038993	0,84	0,0442
1437852_x_at	Cpsf3	cleavage and polyadenylation specificity factor 3	0,85	0,0468
1448483_a_at	Ndufb2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2	0,85	0,0366
1458569_at	Ell2	elongation factor RNA polymerase II 2	0,85	0,0395
1434341_x_at	1110020P15Rik	RIKEN cDNA 1110020P15 gene	0,85	0,0369
1435376_at	Ddhd2	DDHD domain containing 2	0,85	0,0344
1415716_a_at	Rps27	ribosomal protein S27	0,85	0,0275
1449672_s_at	Tufm	Tu translation elongation factor, mitochondrial	0,85	0,0449
1434579_x_at	Ndufs8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	0,85	0,0161
1460523_at	NA	NA	0,85	0,0289
1449575_a_at	Gstp1	glutathione S-transferase, pi 1	0,85	0,0186
1420439_at	Tsx	testis specific X-linked gene	0,85	0,0354
1460361_at	5033414D02Rik	RIKEN cDNA 5033414D02 gene	0,85	0,0180
1449777_at	Dus4l	dihydrouridine synthase 4-like (S. cerevisiae)	0,85	0,0207

1428163_at	Sar1b	SAR1 gene homolog B (S. cerevisiae)	0,85	0,0137
1435729_at	Robld3	roadblock domain containing 3	0,85	0,0479
1444345_at	NA	NA	0,85	0,0264
1437952_at	AU040096	expressed sequence AU040096	0,85	0,0430
1428473_at	Ppp3cb	protein phosphatase 3, catalytic subunit, beta isoform	0,85	0,0417
1426088_at	NA	NA	0,85	0,0419
1450123_at	Ryr2	ryanodine receptor 2, cardiac	0,85	0,0315
1417731_at	Pqbp1	polyglutamine binding protein 1	0,85	0,0279
1435967_s_at	Hibadh	3-hydroxyisobutyrate dehydrogenase	0,85	0,0447
1423096_at	Capn7	calpain 7	0,85	0,0340
1455286_at	Btbd1	BTB (POZ) domain containing 1	0,85	0,0367
1440946_at	NA	NA	0,85	0,0320
1429075_a_at	1700018B08Rik	RIKEN cDNA 1700018B08 gene	0,85	0,0468
1451267_at	Sharpin	SHANK-associated RH domain interacting protein	0,85	0,0386
1457212_at	NA	NA	0,85	0,0494
1452790_x_at	Ndufa3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3	0,85	0,0157
1425064_at	Arnt	aryl hydrocarbon receptor nuclear translocator	0,85	0,0483
1429425_at	Rnf139	ring finger protein 139	0,85	0,0410
1418124_at	Tmem85	transmembrane protein 85	0,85	0,0155
1447714_x_at	NA	NA	0,85	0,0224
1439334_at	NA	NA	0,85	0,0459
1452586_at	Anapc13	anaphase promoting complex subunit 13	0,85	0,0228
1422614_s_at	Bloc1s1	biogenesis of lysosome-related organelles complex-1, subunit 1	0,85	0,0447
1450966_at	Crot	carnitine O-octanoyltransferase	0,85	0,0492
1415980_at	Atp5g2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	0,85	0,0242
1442937_at	C77190	expressed sequence C77190	0,85	0,0443
1451387_s_at	Cuta	cutA divalent cation tolerance homolog (E. coli)	0,85	0,0142
1416278_a_at	Atp5o	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	0,85	0,0130
1422578_at	Cs	citrate synthase	0,85	0,0445
1444998_at	NA	NA	0,85	0,0373
1429901_at	Nkain2	Na+/K+ transporting ATPase interacting 2	0,85	0,0292
1415754_at	Polr2f	polymerase (RNA) II (DNA directed) polypeptide F	0,85	0,0482
1418833_at	Agxt	alanine-glyoxylate aminotransferase	0,85	0,0445
1423737_at	Ndufs3	NADH dehydrogenase (ubiquinone) Fe-S protein 3	0,86	0,0213
1416245_at	Aurkaip1	aurora kinase A interacting protein 1	0,86	0,0240
1456967_at	Trim66	tripartite motif-containing 66	0,86	0,0369
1430713_s_at	Ndufa13	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	0,86	0,0107
1428214_at	Tomm7	translocase of outer mitochondrial membrane 7 homolog (yeast)	0,86	0,0376
1448243_at	Napa	N-ethylmaleimide sensitive fusion protein attachment protein alpha	0,86	0,0330
1418549_at	Cga	glycoprotein hormones, alpha subunit	0,86	0,0364
1423692_at	Ndufa8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8	0,86	0,0063
1422451_at	Mrps21	mitochondrial ribosomal protein S21	0,86	0,0361
1437807_x_at	Ctnna1	catenin (cadherin associated protein), alpha 1	0,86	0,0391
1416834_x_at	Ndufb2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2	0,86	0,0193
1415984_at	Acadm	acyl-Coenzyme A dehydrogenase, medium chain	0,86	0,0412
1428169_at	Atg16l1	autophagy-related 16-like 1 (yeast)	0,86	0,0267
1435201_at	Tmem174	transmembrane protein 174	0,86	0,0333

1428241_at	2310035K24Rik	RIKEN cDNA 2310035K24 gene	0,86	0,0378
1417108_at	Klc4	kinesin light chain 4	0,86	0,0438
1416228_at	Pin1	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1	0,86	0,0405
1426651_at	Mrpl44	mitochondrial ribosomal protein L44	0,86	0,0192
1450818_a_at	Ndufa7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	0,86	0,0290
1416183_a_at	Ldhb	lactate dehydrogenase B	0,86	0,0413
1428553_at	Glrx5	glutaredoxin 5 homolog (S. cerevisiae)	0,86	0,0260
1422976_x_at	Ndufa7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	0,86	0,0482
1451312_at	Ndufs7	NADH dehydrogenase (ubiquinone) Fe-S protein 7	0,86	0,0230
1450055_at	Vsnl1	visinin-like 1	0,86	0,0443
1451673_at	Cd8a	CD8 antigen, alpha chain	0,87	0,0234
1415891_at	Suclg1	succinate-CoA ligase, GDP-forming, alpha subunit	0,87	0,0281
1416534_at	Dpf2	D4, zinc and double PHD fingers family 2	0,87	0,0303
1434213_x_at	Ndufs8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	0,87	0,0483
1416960_at	B3gat3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	0,87	0,0449
1449218_at	Cox8b	cytochrome c oxidase, subunit VIIIb	0,87	0,0446
1432975_at	2310038E17Rik	RIKEN cDNA 2310038E17 gene	0,87	0,0467
1431665_a_at	Timm8b	translocase of inner mitochondrial membrane 8 homolog b (yeast)	0,87	0,0479
1428075_at	Ndufb4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4	0,87	0,0244
1428316_a_at	Fundc2	FUN14 domain containing 2	0,87	0,0368
1449445_x_at	Mfap1a	microfibrillar-associated protein 1A	0,88	0,0491
1416175_a_at	Vdac3	voltage-dependent anion channel 3	0,88	0,0431
1423604_at	Ncan	neurocan	0,88	0,0395
1423857_at	Mrpl30	mitochondrial ribosomal protein L30	0,88	0,0281
1428076_s_at	Ndufb4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4	0,88	0,0325
1425220_x_at	AF067061	cDNA sequence AF067061	0,88	0,0417
1454716_x_at	Cox5b	cytochrome c oxidase, subunit Vb	0,88	0,0472
1416567_s_at	Atp5e	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	0,88	0,0428
1451311_a_at	Adipor1	adiponectin receptor 1	0,88	0,0475
1455235_x_at	Ldhb	lactate dehydrogenase B	0,88	0,0432
1430474_a_at	Mtch2	mitochondrial carrier homolog 2 (C. elegans)	0,88	0,0417
1439017_x_at	Adipor1	adiponectin receptor 1	0,89	0,0387
1423716_s_at	Atp5d	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	0,89	0,0440

Table II

Upregulated in Shunt vs. Sham

Affymetrix probe set identification	Gene symbol	Gene name	Fold change	Adjusted *P* value
1427747_a_at	Lcn2	lipocalin 2	7,34	0,0298
1455905_at	2610507B11Rik	RIKEN cDNA 2610507B11 gene	4,57	0,0061
1419100_at	Serpina3n	serine (or cysteine) peptidase inhibitor, clade A, member 3N	4,45	0,0499
1422660_at	Rbm3	RNA binding motif protein 3	3,97	0,0032
1417355_at	Peg3	paternally expressed 3	3,90	0,0428
1416125_at	Fkbp5	FK506 binding protein 5	3,27	0,0081
1436538_at	Ankrd37	ankyrin repeat domain 37	3,20	0,0299
1428942_at	Mt2	metallothionein 2	3,15	0,0250
1455980_a_at	Gas2l3	growth arrest-specific 2 like 3	3,13	0,0233
1415988_at	Hdlbp	high density lipoprotein (HDL) binding protein	2,76	0,0238
1460227_at	Timp1	tissue inhibitor of metalloproteinase 1	2,70	0,0172
1426808_at	Lgals3	lectin, galactose binding, soluble 3	2,65	0,0062
1417496_at	Cp	ceruloplasmin	2,60	0,0440
1448352_at	Luzp1	leucine zipper protein 1	2,58	0,0079
1422860_at	Nts	neurotensin	2,57	0,0237
1427161_at	Cenpf	centromere protein F	2,52	0,0047
1446947_at	NA	NA	2,51	0,0110
1433992_at	Shroom2	shroom family member 2	2,51	0,0021
1431098_at	Clip1	CAP-GLY domain containing linker protein 1	2,49	0,0411
1435137_s_at	1200016E24Rik	RIKEN cDNA 1200016E24 gene	2,49	0,0499
1425060_s_at	Clip1	CAP-GLY domain containing linker protein 1	2,48	0,0448
1451411_at	Gprc5b	G protein-coupled receptor, family C, group 5, member B	2,48	0,0019
1416121_at	Lox	lysyl oxidase	2,47	0,0086
1427699_a_at	Ptpn11	protein tyrosine phosphatase, non-receptor type 11	2,47	0,0148
1450786_x_at	Pdlim5	PDZ and LIM domain 5	2,45	0,0283
1435716_x_at	Snrpn	small nuclear ribonucleoprotein N	2,44	0,0348
1449615_s_at	Hdlbp	high density lipoprotein (HDL) binding protein	2,43	0,0411
1424542_at	S100a4	S100 calcium binding protein A4	2,42	0,0028
1427311_at	Bptf	bromodomain PHD finger transcription factor	2,38	0,0240
1448260_at	Uchl1	ubiquitin carboxy-terminal hydrolase L1	2,37	0,0257
1456147_at	St8sia6	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	2,31	0,0047
1437581_at	Zfp800	zinc finger protein 800	2,30	0,0399
1423674_at	Usp1	ubiquitin specific peptdiase 1	2,29	0,0103
1427275_at	Smc4	structural maintenance of chromosomes 4	2,28	0,0333
1451064_a_at	Psat1	phosphoserine aminotransferase 1	2,28	0,0177
1459860_x_at	Trim2	tripartite motif-containing 2	2,26	0,0036
1453189_at	Ube2i	ubiquitin-conjugating enzyme E2I	2,25	0,0189
1419754_at	Myo5a	myosin VA	2,22	0,0082
1436431_at	1700025G04Rik	RIKEN cDNA 1700025G04 gene	2,21	0,0220

1423162_s_at	Spred1	sprouty protein with EVH-1 domain 1, related sequence	2,19	0,0203
1456440_s_at	St8sia6	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	2,17	0,0211
1424325_at	Esco1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	2,16	0,0086
1435770_at	Txndc13	thioredoxin domain containing 13	2,14	0,0402
1437244_at	Gas2l3	growth arrest-specific 2 like 3	2,14	0,0341
1430530_s_at	Nmral1	NmrA-like family domain containing 1	2,13	0,0496
1427276_at	Smc4	structural maintenance of chromosomes 4	2,10	0,0111
1449221_a_at	Rrbp1	ribosome binding protein 1	2,09	0,0247
1456112_at	Tpr	translocated promoter region	2,08	0,0088
1417623_at	Slc12a2	solute carrier family 12, member 2	2,07	0,0336
1429156_at	2610036L11Rik	RIKEN cDNA 2610036L11 gene	2,05	0,0255
1438091_a_at	H2afz	H2A histone family, member Z	2,04	0,0264
1426123_a_at	Rrbp1	ribosome binding protein 1	2,04	0,0196
1423594_a_at	Ednrb	endothelin receptor type B	2,02	0,0164
1437118_at	Usp7	ubiquitin specific peptidase 7	2,01	0,0499
1451458_at	Tmem2	transmembrane protein 2	2,00	0,0272
1451667_at	Fam20b	family with sequence similarity 20, member B	1,98	0,0029
1448471_a_at	Ctla2a	cytotoxic T lymphocyte-associated protein 2 alpha	1,97	0,0047
1443230_at	NA	NA	1,94	0,0386
1416077_at	Adm	adrenomedullin	1,93	0,0247
1416342_at	Tnc	tenascin C	1,93	0,0428
1448551_a_at	Trim2	tripartite motif-containing 2	1,93	0,0200
1428936_at	Atp2b1	ATPase, Ca++ transporting, plasma membrane 1	1,92	0,0113
1416544_at	Ezh2	enhancer of zeste homolog 2 (Drosophila)	1,91	0,0221
1417379_at	Iqgap1	IQ motif containing GTPase activating protein 1	1,91	0,0047
1448232_x_at	Tuba1c	tubulin, alpha 1C	1,90	0,0283
1439764_s_at	Igf2bp2	insulin-like growth factor 2 mRNA binding protein 2	1,90	0,0456
1453022_at	Gpihbp1	GPI-anchored HDL-binding protein 1	1,90	0,0024
1439463_x_at	ENSMUSG00000060128	predicted gene, ENSMUSG00000060128	1,89	0,0051
1438556_a_at	Tmod3	tropomodulin 3	1,87	0,0438
1427941_at	Dicer1	Dicer1, Dcr-1 homolog (Drosophila)	1,87	0,0443
1416801_at	Trpm7	transient receptor potential cation channel, subfamily M, member 7	1,86	0,0404
1457744_at	Ddx46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	1,85	0,0164
1415999_at	Hey1	hairy/enhancer-of-split related with YRPW motif 1	1,84	0,0230
1436530_at	OTTMUSG00000000971	predicted gene, OTTMUSG00000000971	1,84	0,0099
1454607_s_at	Psat1	phosphoserine aminotransferase 1	1,84	0,0246
1422861_s_at	Pdlim5	PDZ and LIM domain 5	1,83	0,0298
1450852_s_at	F2r	coagulation factor II (thrombin) receptor	1,83	0,0027
1432216_s_at	Mpp7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	1,83	0,0278
1436343_at	Chd4	chromodomain helicase DNA binding protein 4	1,82	0,0312
1416811_s_at	Ctla2a	cytotoxic T lymphocyte-associated protein 2 alpha	1,81	0,0027
1417507_at	Cyb561	cytochrome b-561	1,80	0,0019
1456262_at	Rbm5	RNA binding motif protein 5	1,79	0,0346
1450397_at	Mtap1b	microtubule-associated protein 1B	1,79	0,0414
1426612_at	Tipin	timeless interacting protein	1,79	0,0019
1435890_at	Atl3	atlastin GTPase 3	1,78	0,0111
1425565_at	Rest	RE1-silencing transcription factor	1,78	0,0227
1447787_x_at	Gjc1	gap junction protein, gamma 1	1,76	0,0147

1424613_at	Gprc5b	G protein-coupled receptor, family C, group 5, member B	1,76	0,0055
1437478_s_at	Efhd2	EF hand domain containing 2	1,75	0,0086
1450864_at	Calm3	calmodulin 3	1,74	0,0164
1448650_a_at	Pole	polymerase (DNA directed), epsilon	1,71	0,0371
1417938_at	Rad51ap1	RAD51 associated protein 1	1,71	0,0410
1428730_at	Krit1	KRIT1, ankyrin repeat containing	1,71	0,0284
1436985_at	Zfp644	zinc finger protein 644	1,71	0,0198
1415895_at	Snrpn	small nuclear ribonucleoprotein N	1,71	0,0357
1440882_at	Lrp8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	1,71	0,0349
1449380_at	Pacsin1	protein kinase C and casein kinase substrate in neurons 1	1,71	0,0048
1452595_at	Adamts4	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 4	1,70	0,0138
1438476_a_at	Chd4	chromodomain helicase DNA binding protein 4	1,69	0,0190
1450845_a_at	Bzw1	basic leucine zipper and W2 domains 1	1,69	0,0141
1444952_a_at	Nucks1	nuclear casein kinase and cyclin-dependent kinase substrate 1	1,69	0,0103
1426259_at	Pank3	pantothenate kinase 3	1,69	0,0350
1441869_x_at	NA	NA	1,69	0,0299
1420985_at	Ash1l	ash1 (absent, small, or homeotic)-like (Drosophila)	1,69	0,0499
1424176_a_at	Anxa4	annexin A4	1,68	0,0337
1437308_s_at	F2r	coagulation factor II (thrombin) receptor	1,68	0,0013
1420843_at	Ptprf	protein tyrosine phosphatase, receptor type, F	1,68	0,0184
1426024_a_at	Dbn1	drebrin 1	1,68	0,0410
1437158_at	Nipbl	Nipped-B homolog (Drosophila)	1,68	0,0413
1450872_s_at	Lipa	lysosomal acid lipase A	1,67	0,0361
1418937_at	Dio2	deiodinase, iodothyronine, type II	1,67	0,0114
1438566_at	St8sia6	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	1,67	0,0081
1437595_at	E030010A14Rik	RIKEN cDNA E030010A14 gene	1,66	0,0109
1428820_at	Mapre1	microtubule-associated protein, RP/EB family, member 1	1,66	0,0435
1449070_x_at	Apcdd1	adenomatosis polyposis coli down-regulated 1	1,66	0,0276
1454822_x_at	Apcdd1	adenomatosis polyposis coli down-regulated 1	1,65	0,0358
1431057_a_at	Prss23	protease, serine, 23	1,65	0,0055
1428301_at	ENSMUSG00000068790	predicted gene, ENSMUSG00000068790	1,64	0,0321
1453572_a_at	Plp2	proteolipid protein 2	1,64	0,0032
1423040_at	Bzw1	basic leucine zipper and W2 domains 1	1,64	0,0303
1434010_at	Fam117b	family with sequence similarity 117, member B	1,63	0,0348
1458464_at	Hecw2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	1,63	0,0410
1418562_at	Sf3b1	splicing factor 3b, subunit 1	1,63	0,0098
1436759_x_at	LOC100047856	similar to calponin 3, acidic	1,63	0,0399
1428228_at	Pgm3	phosphoglucomutase 3	1,62	0,0452
1434020_at	Pdap1	PDGFA associated protein 1	1,62	0,0349
1421375_a_at	S100a6	S100 calcium binding protein A6 (calcyclin)	1,62	0,0063
1455150_at	Hecw2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	1,62	0,0128
1437671_x_at	Prss23	protease, serine, 23	1,62	0,0127
1455732_at	2610510E02Rik	RIKEN cDNA 2610510E02 gene	1,61	0,0086
1457058_at	Adamts2	a disintegrin-like and metallopeptidase (reprolysin type)	1,61	0,0251

		with thrombospondin type 1 motif, 2		
1417028_a_at	Trim2	tripartite motif-containing 2	1,61	0,0391
1420842_at	Ptprf	protein tyrosine phosphatase, receptor type, F	1,60	0,0259
1460230_at	Syn2	synapsin II	1,60	0,0399
1421034_a_at	Il4ra	interleukin 4 receptor, alpha	1,60	0,0081
1452359_at	Rell1	RELT-like 1	1,60	0,0259
1418430_at	Kif5b	kinesin family member 5B	1,59	0,0477
1417872_at	Fhl1	four and a half LIM domains 1	1,59	0,0390
1426326_at	Zfp91	zinc finger protein 91	1,59	0,0448
1460243_at	Sptlc2	serine palmitoyltransferase, long chain base subunit 2	1,59	0,0138
1430820_a_at	Bbx	bobby sox homolog (Drosophila)	1,59	0,0443
1435324_x_at	Hmgb1	high mobility group box 1	1,58	0,0098
1452722_a_at	Cul5	cullin 5	1,58	0,0206
1429384_at	Csnk1g3	casein kinase 1, gamma 3	1,58	0,0355
1427357_at	Cda	cytidine deaminase	1,58	0,0428
1419642_at	Purb	purine rich element binding protein B	1,57	0,0147
1420249_s_at	Ccl6	chemokine (C-C motif) ligand 6	1,57	0,0365
1431339_a_at	Efhd2	EF hand domain containing 2	1,57	0,0347
1421821_at	Ldlr	low density lipoprotein receptor	1,57	0,0295
1456102_a_at	Cul5	cullin 5	1,57	0,0267
1418822_a_at	Arf6	ADP-ribosylation factor 6	1,57	0,0196
1421101_a_at	Ldb2	LIM domain binding 2	1,56	0,0265
1430782_at	Ncapd3	non-SMC condensin II complex, subunit D3	1,56	0,0215
1428976_at	Tmpo	thymopoietin	1,55	0,0021
1455570_x_at	Cnn3	calponin 3, acidic	1,55	0,0391
1456913_at	NA	NA	1,55	0,0087
1458179_at	NA	NA	1,55	0,0499
1433481_at	Fkbp14	FK506 binding protein 14	1,55	0,0081
1451456_at	6430706D22Rik	RIKEN cDNA 6430706D22 gene	1,55	0,0443
1460378_a_at	Tes	testis derived transcript	1,54	0,0279
1452445_at	Slc41a2	solute carrier family 41, member 2	1,54	0,0108
1440991_at	Plekhg1	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	1,54	0,0164
1460238_at	Msln	mesothelin	1,54	0,0392
1422715_s_at	Acp1	acid phosphatase 1, soluble	1,53	0,0499
1420394_s_at	Lilrb4	leukocyte immunoglobulin-like receptor, subfamily B, member 4	1,53	0,0130
1437545_at	Rcor1	REST corepressor 1	1,53	0,0150
1426777_a_at	Wasl	Wiskott-Aldrich syndrome-like (human)	1,53	0,0484
1423161_s_at	Spred1	sprouty protein with EVH-1 domain 1, related sequence	1,53	0,0047
1422764_at	Mapre1	microtubule-associated protein, RP/EB family, member 1	1,52	0,0260
1418245_a_at	Rbm9	RNA binding motif protein 9	1,52	0,0298
1459791_at	Dnajc1	DnaJ (Hsp40) homolog, subfamily C, member 1	1,52	0,0202
1438168_x_at	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	1,52	0,0129
1443768_at	Rhoa	ras homolog gene family, member A	1,52	0,0341
1437087_at	2210408K08Rik	RIKEN cDNA 2210408K08 gene	1,52	0,0028
1433623_at	Zfp367	zinc finger protein 367	1,52	0,0266
1443314_at	Slc12a6	solute carrier family 12, member 6	1,51	0,0238
1449094_at	Gjc1	gap junction protein, gamma 1	1,51	0,0065
1455642_a_at	Tspan17	tetraspanin 17	1,51	0,0051
1449461_at	Rbp7	retinol binding protein 7, cellular	1,51	0,0048
1435749_at	Gda	guanine deaminase	1,51	0,0361
1422062_at	Msr1	macrophage scavenger receptor 1	1,50	0,0341

1417101_at	Hspa2	heat shock protein 2	1,50	0,0247
1430680_a_at	5830417I10Rik	RIKEN cDNA 5830417I10 gene	1,50	0,0432
1424442_a_at	Pja2	praja 2, RING-H2 motif containing	1,49	0,0367
1424609_a_at	100039204	predicted gene, 100039204	1,49	0,0413
1424607_a_at	100039204	predicted gene, 100039204	1,49	0,0488
1436448_a_at	Ptgs1	prostaglandin-endoperoxide synthase 1	1,49	0,0319
1444541_at	NA	NA	1,49	0,0250
1424912_at	Slc25a17	solute carrier family 25 (mitochondrial carrier, peroxisomal membrane protein), member 17	1,49	0,0161
1427953_at	Fanci	Fanconi anemia, complementation group I	1,48	0,0303
1440975_at	Mxra7	matrix-remodelling associated 7	1,48	0,0206
1450157_a_at	Hmmr	hyaluronan mediated motility receptor (RHAMM)	1,48	0,0168
1441683_at	NA	NA	1,48	0,0455
1455814_x_at	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	1,48	0,0256
1453240_a_at	Gcap14	granule cell antiserum positive 14	1,48	0,0166
1426978_at	Klhl2	kelch-like 2, Mayven (Drosophila)	1,48	0,0341
1423228_at	B4galt6	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	1,48	0,0250
1456155_x_at	Hmgcl	3-hydroxy-3-methylglutaryl-Coenzyme A lyase	1,47	0,0228
1419806_at	Hdlbp	high density lipoprotein (HDL) binding protein	1,47	0,0230
1417259_a_at	Capzb	capping protein (actin filament) muscle Z-line, beta	1,47	0,0428
1424708_at	Tmed10	transmembrane emp24-like trafficking protein 10 (yeast)	1,47	0,0410
1434684_at	Rin3	Ras and Rab interactor 3	1,47	0,0220
1434101_at	Nfib	nuclear factor I/B	1,47	0,0468
1437208_at	Sep 10	septin 10	1,46	0,0456
1448744_at	Galns	galactosamine (N-acetyl)-6-sulfate sulfatase	1,46	0,0231
1424110_a_at	Nme1	non-metastatic cells 1, protein (NM23A) expressed in	1,46	0,0139
1434302_at	Raph1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	1,46	0,0329
1425556_at	Crkrs	CDC2-related kinase, arginine/serine-rich	1,45	0,0368
1418823_at	Arf6	ADP-ribosylation factor 6	1,45	0,0280
1451257_at	Acsl6	acyl-CoA synthetase long-chain family member 6	1,45	0,0480
1429327_at	Sdccag1	serologically defined colon cancer antigen 1	1,45	0,0358
1416165_at	Rab31	RAB31, member RAS oncogene family	1,45	0,0341
1438401_at	Ubn1	ubinuclein 1	1,45	0,0222
1433963_a_at	Fermt3	fermitin family homolog 3 (Drosophila)	1,45	0,0255
1429060_at	Malat1	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	1,44	0,0398
1431086_s_at	Pcmt1	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	1,44	0,0169
1422906_at	Abcg2	ATP-binding cassette, sub-family G (WHITE), member 2	1,44	0,0444
1442827_at	Tlr4	toll-like receptor 4	1,44	0,0499
1449870_a_at	Atp6v0a2	ATPase, H+ transporting, lysosomal V0 subunit A2	1,44	0,0473
1460330_at	Anxa3	annexin A3	1,44	0,0442
1458886_at	NA	NA	1,44	0,0373
1440881_at	Brwd3	bromodomain and WD repeat domain containing 3	1,43	0,0289
1423160_at	Spred1	sprouty protein with EVH-1 domain 1, related sequence	1,43	0,0171
1436984_at	Abi2	abl-interactor 2	1,43	0,0180
1435346_at	Ccdc82	coiled-coil domain containing 82	1,43	0,0303
1422555_s_at	Gna13	guanine nucleotide binding protein, alpha 13	1,43	0,0284
1416335_at	Mif	macrophage migration inhibitory factor	1,43	0,0088
1460671_at	Gpx1	glutathione peroxidase 1	1,43	0,0059
1420832_at	Qsox1	quiescin Q6 sulfhydryl oxidase 1	1,42	0,0028

1425148_a_at	Snx6	sorting nexin 6	1,42	0,0032
1423596_at	Nek6	NIMA (never in mitosis gene a)-related expressed kinase 6	1,42	0,0270
1424065_at	Edem1	ER degradation enhancer, mannosidase alpha-like 1	1,42	0,0168
1421477_at	Cplx2	complexin 2	1,42	0,0086
1420715_a_at	Pparg	peroxisome proliferator activated receptor gamma	1,42	0,0081
1424940_s_at	BC022687	cDNA sequence BC022687	1,42	0,0249
1428574_a_at	Chn2	chimerin (chimaerin) 2	1,42	0,0081
1427299_at	Rps6ka3	ribosomal protein S6 kinase polypeptide 3	1,41	0,0238
1436738_at	Pif1	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae)	1,41	0,0298
1430151_at	Nisch	nischarin	1,41	0,0448
1424398_at	Dhx36	DEAH (Asp-Glu-Ala-His) box polypeptide 36	1,41	0,0200
1450011_at	Hsd17b12	hydroxysteroid (17-beta) dehydrogenase 12	1,41	0,0221
1418296_at	Fxyd5	FXYD domain-containing ion transport regulator 5	1,41	0,0125
1441618_at	Arhgap29	Rho GTPase activating protein 29	1,41	0,0171
1428527_at	Snx7	sorting nexin 7	1,41	0,0047
1452268_at	Fam76b	family with sequence similarity 76, member B	1,41	0,0430
1421947_at	Gng12	guanine nucleotide binding protein (G protein), gamma 12	1,40	0,0187
1455859_at	A330021E22Rik	RIKEN cDNA A330021E22 gene	1,40	0,0438
1422878_at	Syt12	synaptotagmin XII	1,40	0,0482
1419301_at	Fzd4	frizzled homolog 4 (Drosophila)	1,40	0,0499
1423877_at	Chaf1b	chromatin assembly factor 1, subunit B (p60)	1,40	0,0381
1438771_at	Brd1	bromodomain containing 1	1,40	0,0299
1422778_at	Taf9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor	1,40	0,0147
1450878_at	Sri	sorcin	1,40	0,0185
1436986_at	Sntb2	syntrophin, basic 2	1,40	0,0086
1425460_at	Mtmr2	myotubularin related protein 2	1,39	0,0413
1429185_at	4631416L12Rik	RIKEN cDNA 4631416L12 gene	1,39	0,0255
1428971_at	Ccny	cyclin Y	1,39	0,0196
1428889_at	Alkbh3	alkB, alkylation repair homolog 3 (E. coli)	1,39	0,0189
1417124_at	Dstn	destrin	1,39	0,0496
1437937_at	Ccbp2	chemokine binding protein 2	1,39	0,0366
1437642_at	Agfg2	ArfGAP with FG repeats 2	1,39	0,0283
1456274_at	C230071H18Rik	RIKEN cDNA C230071H18 gene	1,39	0,0308
1446272_at	Pctk2	PCTAIRE-motif protein kinase 2	1,39	0,0443
1425523_at	Rbm25	RNA binding motif protein 25	1,39	0,0497
1418382_at	Apcdd1	adenomatosis polyposis coli down-regulated 1	1,38	0,0399
1425603_at	Tmem176a	transmembrane protein 176A	1,38	0,0065
1426710_at	Calm3	calmodulin 3	1,38	0,0128
1419640_at	Purb	purine rich element binding protein B	1,38	0,0428
1424309_a_at	Mocs2	molybdenum cofactor synthesis 2	1,38	0,0251
1448129_at	Arpc5	actin related protein 2/3 complex, subunit 5	1,38	0,0352
1449821_a_at	Memo1	mediator of cell motility 1	1,37	0,0021
1426985_s_at	Fam76b	family with sequence similarity 76, member B	1,37	0,0427
1439481_at	Ipo9	importin 9	1,37	0,0298
1436063_at	Loxl1	lysyl oxidase-like 1	1,37	0,0396
1426523_a_at	Gnpda2	glucosamine-6-phosphate deaminase 2	1,37	0,0257
1418097_a_at	Crlf2	cytokine receptor-like factor 2	1,37	0,0114
1442623_at	NA	NA	1,37	0,0196
1447602_x_at	Sulf2	sulfatase 2	1,37	0,0438

1421223_a_at	Anxa4	annexin A4	1,37	0,0177
1418963_at	2310047O13Rik	RIKEN cDNA 2310047O13 gene	1,36	0,0109
1421814_at	Msn	moesin	1,36	0,0315
1434248_at	Prkch	protein kinase C, eta	1,36	0,0298
1443626_at	NA	NA	1,36	0,0444
1455649_at	Ttc9	tetratricopeptide repeat domain 9	1,36	0,0256
1446904_at	NA	NA	1,36	0,0415
1439555_at	Rlf	rearranged L-myc fusion sequence	1,36	0,0391
1417027_at	Trim2	tripartite motif-containing 2	1,36	0,0365
1457180_at	Dip2c	DIP2 disco-interacting protein 2 homolog C (Drosophila)	1,35	0,0491
1423643_at	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	1,35	0,0443
1448339_at	Tmem30a	transmembrane protein 30A	1,35	0,0430
1424318_at	1110067D22Rik	RIKEN cDNA 1110067D22 gene	1,35	0,0452
1448736_a_at	Hprt1	hypoxanthine guanine phosphoribosyl transferase 1	1,35	0,0171
1434378_a_at	NA	NA	1,35	0,0379
1417571_at	Mpg	N-methylpurine-DNA glycosylase	1,34	0,0499
1426392_a_at	Actr3	ARP3 actin-related protein 3 homolog (yeast)	1,34	0,0486
1441848_at	NA	NA	1,34	0,0361
1416695_at	Tspo	translocator protein	1,34	0,0332
1451122_at	Idi1	isopentenyl-diphosphate delta isomerase	1,34	0,0270
1416066_at	Cd9	CD9 antigen	1,34	0,0306
1435737_a_at	Nde1	nuclear distribution gene E homolog 1 (A nidulans)	1,34	0,0081
1444642_at	NA	NA	1,34	0,0416
1448638_at	Mtbp	Mdm2, transformed 3T3 cell double minute p53 binding protein	1,34	0,0383
1448879_at	Ube2l3	ubiquitin-conjugating enzyme E2L 3	1,34	0,0452
1449256_a_at	Rab11a	RAB11a, member RAS oncogene family	1,33	0,0042
1425950_at	Slc17a9	solute carrier family 17, member 9	1,33	0,0464
1427266_at	Pbrm1	polybromo 1	1,33	0,0422
1424334_at	Tspan17	tetraspanin 17	1,33	0,0256
1449396_at	Aoc3	amine oxidase, copper containing 3	1,32	0,0452
1436900_x_at	Leprot	leptin receptor overlapping transcript	1,32	0,0443
1454743_at	Nup205	nucleoporin 205	1,32	0,0422
1458025_at	NA	NA	1,32	0,0209
1427939_s_at	Mycbp	c-myc binding protein	1,31	0,0144
1448953_at	Blm	Bloom syndrome homolog (human)	1,31	0,0342
1454353_at	4833420D23Rik	RIKEN cDNA 4833420D23 gene	1,31	0,0347
1426461_at	Ugp2	UDP-glucose pyrophosphorylase 2	1,31	0,0213
1460428_at	Ankrd13a	ankyrin repeat domain 13a	1,31	0,0391
1418905_at	Nubp1	nucleotide binding protein 1	1,31	0,0294
1435277_x_at	Nme1	non-metastatic cells 1, protein (NM23A) expressed in	1,31	0,0438
1419737_a_at	Ldha	lactate dehydrogenase A	1,31	0,0262
1453298_at	Ptpn21	protein tyrosine phosphatase, non-receptor type 21	1,31	0,0413
1420376_a_at	H3f3b	H3 histone, family 3B	1,30	0,0283
1437635_at	St3gal6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	1,30	0,0237
1456727_a_at	Csnk1d	casein kinase 1, delta	1,30	0,0375
1435771_at	Plcb4	phospholipase C, beta 4	1,30	0,0499
1415778_at	Morf4l2	mortality factor 4 like 2	1,30	0,0184
1452983_at	Cep57	centrosomal protein 57	1,30	0,0255
1454727_at	Afap1l1	actin filament associated protein 1-like 1	1,30	0,0284
1452649_at	Rtn4	reticulon 4	1,30	0,0100
1449323_a_at	Rpl3	ribosomal protein L3	1,30	0,0078
1430575_a_at	Tpp2	tripeptidyl peptidase II	1,30	0,0426

1457416_at	NA	NA	1,29	0,0147
1459616_at	NA	NA	1,29	0,0461
1438665_at	Smpd3	sphingomyelin phosphodiesterase 3, neutral	1,29	0,0430
1428554_a_at	1810035L17Rik	RIKEN cDNA 1810035L17 gene	1,29	0,0069
1423383_a_at	Osbpl9	oxysterol binding protein-like 9	1,29	0,0216
1425553_s_at	Hip1r	huntingtin interacting protein 1 related	1,29	0,0155
1445210_at	NA	NA	1,29	0,0465
1417817_a_at	Wwtr1	WW domain containing transcription regulator 1	1,29	0,0199
1423369_at	Fmr1	fragile X mental retardation syndrome 1 homolog	1,28	0,0478
1441825_x_at	Ighmbp2	immunoglobulin mu binding protein 2	1,28	0,0381
1430193_at	Casc5	cancer susceptibility candidate 5	1,28	0,0391
1428738_a_at	D14Ertd449e	DNA segment, Chr 14, ERATO Doi 449, expressed	1,28	0,0238
1424910_at	Kif12	kinesin family member 12	1,28	0,0306
1418451_at	Gng2	guanine nucleotide binding protein (G protein), gamma 2	1,28	0,0238
1455249_at	NA	NA	1,28	0,0321
1448903_at	Sep 15	selenoprotein	1,28	0,0138
1438629_x_at	Grn	granulin	1,28	0,0381
1439888_at	NA	NA	1,27	0,0312
1454056_at	9030407P20Rik	RIKEN cDNA 9030407P20 gene	1,27	0,0410
1438137_at	NA	NA	1,27	0,0442
1441138_at	Foxn2	forkhead box N2	1,26	0,0468
1418703_at	Rbms1	RNA binding motif, single stranded interacting protein 1	1,26	0,0079
1437867_at	NA	NA	1,26	0,0422
1433027_at	5830485P09Rik	RIKEN cDNA 5830485P09 gene	1,26	0,0428
1450117_at	Tcf3	transcription factor 3	1,26	0,0361
1437148_at	Arpc2	actin related protein 2/3 complex, subunit 2	1,25	0,0174
1428452_at	2810025M15Rik	RIKEN cDNA 2810025M15 gene	1,25	0,0103
1446311_at	Mbc2	membrane bound C2 domain containing protein	1,25	0,0302
1418355_at	Nucb2	nucleobindin 2	1,25	0,0440
1417418_s_at	Cox6a1	cytochrome c oxidase, subunit VI a, polypeptide 1	1,25	0,0406
1460177_at	Cndp2	CNDP dipeptidase 2 (metallopeptidase M20 family)	1,25	0,0478
1417023_a_at	Fabp4	fatty acid binding protein 4, adipocyte	1,25	0,0200
1423132_a_at	5730427N09Rik	RIKEN cDNA 5730427N09 gene	1,25	0,0396
1446027_at	NA	NA	1,24	0,0410
1455801_x_at	Tbcd	tubulin-specific chaperone d	1,24	0,0200
1417291_at	Tnfrsf1a	tumor necrosis factor receptor superfamily, member 1a	1,24	0,0137
1416093_a_at	Mrpl20	mitochondrial ribosomal protein L20	1,24	0,0164
1426759_at	Map4k3	mitogen-activated protein kinase kinase kinase kinase 3	1,24	0,0229
1422553_at	Pten	phosphatase and tensin homolog	1,24	0,0287
1436335_at	Plch2	phospholipase C, eta 2	1,24	0,0306
1426397_at	Tgfbr2	transforming growth factor, beta receptor II	1,23	0,0456
1424438_a_at	Leprot	leptin receptor overlapping transcript	1,23	0,0398
1456567_x_at	Grn	granulin	1,23	0,0413
1416435_at	Ltbr	lymphotoxin B receptor	1,22	0,0499
1448524_s_at	Ssr4	signal sequence receptor, delta	1,22	0,0214
1417464_at	Tnnc2	troponin C2, fast	1,22	0,0379
1434968_a_at	Actr3	ARP3 actin-related protein 3 homolog (yeast)	1,22	0,0385
1416027_at	Pdcd6	programmed cell death 6	1,22	0,0172
1421663_at	Dhrs2	dehydrogenase/reductase member 2	1,22	0,0301

1416241_at	Sec13	SEC13 homolog (S. cerevisiae)	1,21	0,0449
1422507_at	Cstb	cystatin B	1,20	0,0440
1419305_a_at	Fbxo36	F-box protein 36	1,20	0,0493
1424432_at	Ubtd1	ubiquitin domain containing 1	1,20	0,0484
1460639_a_at	Atox1	ATX1 (antioxidant protein 1) homolog 1 (yeast)	1,19	0,0428

Downregulated in Shunt vs. Sham

Affymetrix probe set identification	Gene symbol	Gene name	Fold change	Adjusted *P* value
1452388_at	Hspa1a	heat shock protein 1A	0,18	0,0256
1427126_at	Hspa1b	heat shock protein 1B	0,18	0,0203
1427127_x_at	Hspa1b	heat shock protein 1B	0,22	0,0310
1452318_a_at	Hspa1b	heat shock protein 1B	0,23	0,0394
1423566_a_at	Hsph1	heat shock 105kDa/110kDa protein 1	0,24	0,0365
1425993_a_at	Hsph1	heat shock 105kDa/110kDa protein 1	0,25	0,0284
1435290_x_at	H2-Aa	histocompatibility 2, class II antigen A, alpha	0,26	0,0375
1435370_a_at	Ces3	carboxylesterase 3	0,26	0,0019
1440096_at	Ecm2	extracellular matrix protein 2, female organ and adipocyte specific	0,27	0,0413
1418174_at	Dbp	D site albumin promoter binding protein	0,28	0,0368
1438211_s_at	Dbp	D site albumin promoter binding protein	0,29	0,0161
1435574_at	NA	NA	0,29	0,0139
1449081_at	Ces3	carboxylesterase 3	0,30	0,0019
1418849_x_at	Aqp7	aquaporin 7	0,30	0,0189
1436550_at	Fbxo30	F-box protein 30	0,31	0,0237
1458081_at	NA	NA	0,31	0,0238
1449015_at	Retnla	resistin like alpha	0,32	0,0081
1444153_at	NA	NA	0,33	0,0028
1426672_at	Ano10	anoctamin 10	0,33	0,0078
1454850_at	Tbc1d10c	TBC1 domain family, member 10c	0,35	0,0365
1425425_a_at	Wif1	Wnt inhibitory factor 1	0,36	0,0428
1457472_at	Gigyf2	GRB10 interacting GYF protein 2	0,36	0,0151
1425519_a_at	Cd74	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	0,38	0,0308
1439837_at	Gigyf2	GRB10 interacting GYF protein 2	0,38	0,0203
1429639_at	Prei4	preimplantation protein 4	0,38	0,0490
1435371_x_at	Ces3	carboxylesterase 3	0,39	0,0086
1425477_x_at	H2-Ab1	histocompatibility 2, class II antigen A, beta 1	0,40	0,0443
1459835_s_at	Dnaja1	DnaJ (Hsp40) homolog, subfamily A, member 1	0,41	0,0499
1418565_at	Serbp1	serpine1 mRNA binding protein 1	0,41	0,0337
1455358_at	A2bp1	ataxin 2 binding protein 1	0,42	0,0217
1450648_s_at	Rmcs5	response to metastatic cancers 5	0,42	0,0291
1445632_at	Ogdh	oxoglutarate dehydrogenase (lipoamide)	0,43	0,0081
1425115_at	Rbbp6	retinoblastoma binding protein 6	0,44	0,0061
1460179_at	Dnaja1	DnaJ (Hsp40) homolog, subfamily A, member 1	0,45	0,0367
1424952_at	Ociad1	OCIA domain containing 1	0,45	0,0047
1438423_at	Ssbp2	single-stranded DNA binding protein 2	0,45	0,0039
1440443_at	E030016H06Rik	RIKEN cDNA E030016H06 gene	0,45	0,0499
1422155_at	Hist2h3c2	histone cluster 2, H3c2	0,45	0,0337
1435605_at	Actr3b	ARP3 actin-related protein 3 homolog B (yeast)	0,46	0,0334
1444086_at	E030049G20Rik	RIKEN cDNA E030049G20 gene	0,47	0,0093
1435328_at	Cyhr1	cysteine and histidine rich 1	0,47	0,0444
1458218_s_at	Pde7a	phosphodiesterase 7A	0,47	0,0323
1433532_a_at	Mbp	myelin basic protein	0,47	0,0204
1454966_at	Itga8	integrin alpha 8	0,47	0,0438

1449356_at	Asb5	ankyrin repeat and SOCs box-containing 5	0,47	0,0499
1434629_at	Zbtb26	zinc finger and BTB domain containing 26	0,48	0,0139
1440195_at	Serbp1	serpine1 mRNA binding protein 1	0,48	0,0172
1440537_at	Kcnv2	potassium channel, subfamily V, member 2	0,48	0,0024
1438385_s_at	Gpt2	glutamic pyruvate transaminase (alanine aminotransferase) 2	0,48	0,0373
1455475_at	3110057O12Rik	RIKEN cDNA 3110057O12 gene	0,48	0,0169
1441305_at	Nedd4l	neural precursor cell expressed, developmentally down-regulated gene 4-like	0,48	0,0161
1425280_at	Leng1	leukocyte receptor cluster (LRC) member 1	0,48	0,0028
1416839_at	Mut	methylmalonyl-Coenzyme A mutase	0,48	0,0491
1429260_at	1190007I07Rik	RIKEN cDNA 1190007I07 gene	0,49	0,0335
1424716_at	Retsat	retinol saturase (all trans retinol 13,14 reductase)	0,49	0,0273
1436478_at	1810013L24Rik	RIKEN cDNA 1810013L24 gene	0,49	0,0088
1424078_s_at	Pex6	peroxisomal biogenesis factor 6	0,49	0,0083
1427410_at	Dleu2	deleted in lymphocytic leukemia, 2	0,49	0,0214
1457832_at	NA	NA	0,49	0,0028
1453783_at	6330411E07Rik	RIKEN cDNA 6330411E07 gene	0,49	0,0028
1439484_at	Pde7a	phosphodiesterase 7A	0,49	0,0088
1443932_at	Klhdc1	kelch domain containing 1	0,50	0,0150
1420796_at	Ahrr	aryl-hydrocarbon receptor repressor	0,50	0,0234
1455785_at	Kcna1	potassium voltage-gated channel, shaker-related subfamily, member 1	0,50	0,0047
1429021_at	Epha4	Eph receptor A4	0,50	0,0028
1416147_at	Hspa4	heat shock protein 4	0,50	0,0140
1421278_s_at	Spna1	spectrin alpha 1	0,50	0,0145
1443183_at	Huwe1	HECT, UBA and WWE domain containing 1	0,50	0,0114
1436590_at	Ppp1r3b	protein phosphatase 1, regulatory (inhibitor) subunit 3B	0,50	0,0113
1440435_at	Ky	kyphoscoliosis peptidase	0,50	0,0065
1424455_at	Gprasp1	G protein-coupled receptor associated sorting protein 1	0,51	0,0019
1450770_at	3632451O06Rik	RIKEN cDNA 3632451O06 gene	0,51	0,0086
1441751_at	AW493563	expressed sequence AW493563	0,51	0,0477
1439015_at	Gfra1	glial cell line derived neurotrophic factor family receptor alpha 1	0,51	0,0019
1422540_at	Fbln1	fibulin 1	0,51	0,0196
1444305_at	Myh7b	myosin, heavy chain 7B, cardiac muscle, beta	0,51	0,0048
1457671_at	9330120H11Rik	RIKEN cDNA 9330120H11 gene	0,51	0,0161
1456824_at	Zfp612	zinc finger protein 612	0,51	0,0103
1458324_x_at	NA	NA	0,51	0,0114
1429131_at	Ube2v2	ubiquitin-conjugating enzyme E2 variant 2	0,52	0,0299
1433935_at	AU020206	expressed sequence AU020206	0,52	0,0471
1419286_s_at	Ift81	intraflagellar transport 81 homolog (Chlamydomonas)	0,52	0,0021
1452623_at	Zfp759	zinc finger protein 759	0,52	0,0161
1447693_s_at	Neo1	neogenin	0,52	0,0041
1434243_s_at	Tomm70a	translocase of outer mitochondrial membrane 70 homolog A (yeast)	0,52	0,0361
1455025_at	Paqr9	progestin and adipoQ receptor family member IX	0,52	0,0200
1440840_at	D630004K10Rik	RIKEN cDNA D630004K10 gene	0,52	0,0138
1438916_x_at	6720401G13Rik	RIKEN cDNA 6720401G13 gene	0,53	0,0019
1437987_at	NA	NA	0,53	0,0196

1457338_at	NA	NA	0,53	0,0021
1439994_at	NA	NA	0,53	0,0024
1460589_at	Zfp597	zinc finger protein 597	0,53	0,0235
1428487_s_at	Coq10b	coenzyme Q10 homolog B (S. cerevisiae)	0,53	0,0351
1458595_at	Intu	inturned planar cell polarity effector homolog (Drosophila)	0,53	0,0308
1444956_at	NA	NA	0,53	0,0106
1434647_at	Egflam	EGF-like, fibronectin type III and laminin G domains	0,53	0,0079
1437400_at	Nedd4l	neural precursor cell expressed, developmentally down-regulated gene 4-like	0,53	0,0140
1450933_at	Pde7a	phosphodiesterase 7A	0,53	0,0308
1448657_a_at	Dnajb2	DnaJ (Hsp40) homolog, subfamily B, member 2	0,54	0,0132
1456041_at	Snx16	sorting nexin 16	0,54	0,0061
1449407_at	Ift81	intraflagellar transport 81 homolog (Chlamydomonas)	0,54	0,0048
1439790_at	Serpinb9	serine (or cysteine) peptidase inhibitor, clade B, member 9	0,54	0,0210
1423841_at	Bxdc2	brix domain containing 2	0,54	0,0246
1444726_at	Krr1	KRR1, small subunit (SSU) processome component, homolog (yeast)	0,54	0,0177
1455028_at	Mapt	microtubule-associated protein tau	0,54	0,0308
1441139_at	ENSMUSG00000071543	predicted gene, ENSMUSG00000071543	0,55	0,0079
1459325_at	NA	NA	0,55	0,0237
1447500_at	Cux2	cut-like homeobox 2	0,55	0,0426
1438217_at	A2bp1	ataxin 2 binding protein 1	0,55	0,0398
1435714_x_at	Il17d	interleukin 17D	0,55	0,0133
1427251_at	Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	0,55	0,0027
1453566_at	Prr8	proline rich 8	0,55	0,0065
1438803_s_at	Snx16	sorting nexin 16	0,56	0,0250
1424211_at	Slc25a33	solute carrier family 25, member 33	0,56	0,0442
1428870_at	Nolc1	nucleolar and coiled-body phosphoprotein 1	0,56	0,0108
1428791_at	Ube2h	ubiquitin-conjugating enzyme E2H	0,56	0,0030
1449556_at	H2-T23	histocompatibility 2, T region locus 23	0,56	0,0150
1455690_at	NA	NA	0,56	0,0391
1449001_at	Ivd	isovaleryl coenzyme A dehydrogenase	0,56	0,0042
1444224_at	NA	NA	0,56	0,0448
1455961_at	NA	NA	0,56	0,0081
1457440_at	Sstr4	somatostatin receptor 4	0,56	0,0196
1434826_at	Rfesd	Rieske (Fe-S) domain containing	0,56	0,0284
1424834_s_at	Itpr2	inositol 1,4,5-triphosphate receptor 2	0,56	0,0097
1419702_at	Taf1a	TATA box binding protein (Tbp)-associated factor, RNA polymerase I, A	0,56	0,0053
1439821_at	Lrp2bp	Lrp2 binding protein	0,57	0,0112
1423753_at	Bambi	BMP and activin membrane-bound inhibitor, homolog (Xenopus laevis)	0,57	0,0177
1444640_at	Pigg	phosphatidylinositol glycan anchor biosynthesis, class G	0,57	0,0300
1438413_at	Senp7	SUMO1/sentrin specific peptidase 7	0,57	0,0050
1435170_at	Tsr2	TSR2, 20S rRNA accumulation, homolog (S. cerevisiae)	0,57	0,0048
1455459_at	Prdm15	PR domain containing 15	0,58	0,0056
1439511_at	Cdk7	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	0,58	0,0031
1449398_at	Rpl3l	ribosomal protein L3-like	0,58	0,0041
1455337_at	Fgd4	FYVE, RhoGEF and PH domain containing 4	0,58	0,0233

1442640_at	Slfn5	schlafen 5	0,58	0,0407
1434457_at	Sp100	nuclear antigen Sp100	0,58	0,0172
1419056_at	Rtn2	reticulon 2 (Z-band associated protein)	0,58	0,0019
1453232_at	Calr3	calreticulin 3	0,58	0,0028
1454738_x_at	Pex6	peroxisomal biogenesis factor 6	0,58	0,0212
1460033_at	A330023F24Rik	RIKEN cDNA A330023F24 gene	0,58	0,0444
1440954_at	NA	NA	0,58	0,0155
1455492_at	B330016D10Rik	RIKEN cDNA B330016D10 gene	0,58	0,0293
1429108_at	Msl2	male-specific lethal 2 homolog (Drosophila)	0,58	0,0266
1459813_at	1700012D01Rik	RIKEN cDNA 1700012D01 gene	0,58	0,0435
1452238_at	Agfg1	ArfGAP with FG repeats 1	0,58	0,0212
1451212_at	Ccdc21	coiled-coil domain containing 21	0,58	0,0326
1434931_at	Neo1	neogenin	0,58	0,0086
1415911_at	Impact	imprinted and ancient	0,59	0,0191
1423085_at	Efnb3	ephrin B3	0,59	0,0121
1449331_a_at	Rapsn	receptor-associated protein of the synapse	0,59	0,0150
1457473_at	Chd1	chromodomain helicase DNA binding protein 1	0,59	0,0407
1440027_at	NA	NA	0,59	0,0067
1455059_at	Helz	helicase with zinc finger domain	0,59	0,0021
1438930_s_at	Mecp2	methyl CpG binding protein 2	0,59	0,0021
1431126_a_at	0610011F06Rik	RIKEN cDNA 0610011F06 gene	0,59	0,0019
1434170_at	Wdr40b	WD repeat domain 40B	0,59	0,0094
1427104_at	Zfp612	zinc finger protein 612	0,59	0,0027
1445398_at	NA	NA	0,59	0,0140
1455014_at	Hint3	histidine triad nucleotide binding protein 3	0,59	0,0081
1436070_at	Glo1	glyoxalase 1	0,59	0,0131
1449141_at	Fblim1	filamin binding LIM protein 1	0,59	0,0448
1435603_at	Sned1	sushi, nidogen and EGF-like domains 1	0,59	0,0047
1449121_at	Fusip1	FUS interacting protein (serine-arginine rich) 1	0,59	0,0413
1418389_at	2810453I06Rik	RIKEN cDNA 2810453I06 gene	0,59	0,0096
1420342_at	Gdap10	ganglioside-induced differentiation-associated-protein 10	0,59	0,0303
1433509_s_at	Reep1	receptor accessory protein 1	0,59	0,0375
1421277_at	Spna1	spectrin alpha 1	0,59	0,0128
1451226_at	Pex6	peroxisomal biogenesis factor 6	0,59	0,0164
1436028_at	Tmem33	transmembrane protein 33	0,60	0,0071
1434581_at	2410066E13Rik	RIKEN cDNA 2410066E13 gene	0,60	0,0444
1455182_at	Kif1b	kinesin family member 1B	0,60	0,0314
1460225_at	Mrp63	mitochondrial ribosomal protein 63	0,60	0,0046
1420535_a_at	Nub1	negative regulator of ubiquitin-like proteins 1	0,60	0,0135
1436568_at	Jam2	junction adhesion molecule 2	0,60	0,0216
1442371_at	Lmbr1	limb region 1	0,60	0,0167
1441577_at	C530014P21Rik	RIKEN cDNA C530014P21 gene	0,60	0,0021
1434520_at	Sc5d	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae)	0,60	0,0368
1435893_at	Vldlr	very low density lipoprotein receptor	0,60	0,0024
1439777_at	Cugbp2	CUG triplet repeat, RNA binding protein 2	0,60	0,0264
1438878_at	6430537K16Rik	RIKEN cDNA 6430537K16 gene	0,60	0,0024
1424276_at	Snx16	sorting nexin 16	0,60	0,0055

1438041_at	Pde7a	phosphodiesterase 7A	0,60	0,0041
1418585_at	Ccnh	cyclin H	0,60	0,0473
1433806_x_at	Calr	calreticulin	0,60	0,0341
1423365_at	Cacna1g	calcium channel, voltage-dependent, T type, alpha 1G subunit	0,60	0,0168
1443822_s_at	Cisd1	CDGSH iron sulfur domain 1	0,60	0,0426
1430485_at	Trpc2	transient receptor potential cation channel, subfamily C, member 2	0,60	0,0130
1424485_at	Angptl3	angiopoietin-like 3	0,60	0,0299
1435911_s_at	Slc2a12	solute carrier family 2 (facilitated glucose transporter), member 12	0,61	0,0196
1440343_at	Rps6ka5	ribosomal protein S6 kinase, polypeptide 5	0,61	0,0078
1449480_at	Sap18	Sin3-associated polypeptide 18	0,61	0,0389
1440592_at	NA	NA	0,61	0,0053
1445421_at	NA	NA	0,61	0,0446
1449576_at	Eif1ay	eukaryotic translation initiation factor 1A, Y-linked	0,61	0,0399
1423313_at	Pde7a	phosphodiesterase 7A	0,61	0,0139
1445270_at	NA	NA	0,61	0,0041
1434592_at	Slc16a10	solute carrier family 16 (monocarboxylic acid transporters), member 10	0,61	0,0138
1417606_a_at	Calr	calreticulin	0,61	0,0323
1446844_at	Chchd7	coiled-coil-helix-coiled-coil-helix domain containing 7	0,61	0,0028
1417555_at	Atad1	ATPase family, AAA domain containing 1	0,61	0,0198
1427984_at	Senp6	SUMO/sentrin specific peptidase 6	0,61	0,0375
1456625_at	Aasdhppt	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	0,61	0,0141
1442648_at	Zfp563	zinc finger protein 563	0,61	0,0118
1437496_at	Acad10	acyl-Coenzyme A dehydrogenase family, member 10	0,61	0,0129
1424726_at	Tmem150	transmembrane protein 150	0,61	0,0485
1415772_at	Ncl	nucleolin	0,61	0,0496
1418983_at	Inadl	InaD-like (Drosophila)	0,61	0,0047
1448870_at	Ltbp1	latent transforming growth factor beta binding protein 1	0,61	0,0020
1457373_at	NA	NA	0,61	0,0130
1454967_at	NA	NA	0,61	0,0028
1439836_at	Asb15	ankyrin repeat and SOCS box-containing 15	0,61	0,0021
1438971_x_at	Ube2h	ubiquitin-conjugating enzyme E2H	0,61	0,0041
1418186_at	Gstt1	glutathione S-transferase, theta 1	0,61	0,0107
1438520_at	Slc25a36	solute carrier family 25, member 36	0,61	0,0430
1418219_at	Il15	interleukin 15	0,61	0,0055
1436636_at	NA	NA	0,62	0,0171
1456170_x_at	Calr	calreticulin	0,62	0,0375
1416958_at	Nr1d2	nuclear receptor subfamily 1, group D, member 2	0,62	0,0399
1447864_s_at	Pogk	pogo transposable element with KRAB domain	0,62	0,0375
1457966_at	NA	NA	0,62	0,0299
1454855_at	Magi2	membrane associated guanylate kinase, WW and PDZ domain containing 2	0,62	0,0128
1455506_at	Slc25a34	solute carrier family 25, member 34	0,62	0,0173
1435658_at	Slc27a1	solute carrier family 27 (fatty acid transporter), member 1	0,62	0,0178
1443848_at	NA	NA	0,62	0,0428
1438025_at	Mtrf1l	mitochondrial translational release factor 1-like	0,62	0,0282
1430650_at	Zfp191	zinc finger protein 191	0,62	0,0129
1434771_at	0610011F06Rik	RIKEN cDNA 0610011F06 gene	0,62	0,0057
1448529_at	Thbd	thrombomodulin	0,62	0,0111
1455558_at	Ncrna00153	non-protein coding RNA 153	0,62	0,0048

1423112_at	Ube2d3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	0,62	0,0385
1451991_at	Epha7	Eph receptor A7	0,62	0,0086
1455073_at	Cdadc1	cytidine and dCMP deaminase domain containing 1	0,62	0,0029
1451542_at	Ssbp2	single-stranded DNA binding protein 2	0,62	0,0028
1417823_at	Gcat	glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	0,62	0,0053
1436839_at	2010109K11Rik	RIKEN cDNA 2010109K11 gene	0,62	0,0145
1453487_at	Dhdh	dihydrodiol dehydrogenase (dimeric)	0,63	0,0128
1446421_at	NA	NA	0,63	0,0276
1435117_a_at	Dnajc27	DnaJ (Hsp40) homolog, subfamily C, member 27	0,63	0,0152
1447830_s_at	Rgs2	regulator of G-protein signaling 2	0,63	0,0136
1454014_a_at	Mkks	McKusick-Kaufman syndrome protein	0,63	0,0130
1429024_at	Rbm20	RNA binding motif protein 20	0,63	0,0130
1447416_at	Gm239	gene model 239, (NCBI)	0,63	0,0236
1438915_at	6720401G13Rik	RIKEN cDNA 6720401G13 gene	0,63	0,0144
1453135_at	Fndc5	fibronectin type III domain containing 5	0,63	0,0398
1449662_at	Reep1	receptor accessory protein 1	0,63	0,0087
1446524_at	NA	NA	0,63	0,0107
1424833_at	Itpr2	inositol 1,4,5-triphosphate receptor 2	0,63	0,0048
1427620_at	Cul9	cullin 9	0,63	0,0325
1428882_at	Wipi2	WD repeat domain, phosphoinositide interacting 2	0,63	0,0384
1428892_at	Ppil1	peptidylprolyl isomerase (cyclophilin)-like 1	0,63	0,0247
1440187_at	Taf3	TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0,63	0,0127
1455121_at	Lcor	ligand dependent nuclear receptor corepressor	0,63	0,0160
1436678_at	Sgcb	sarcoglycan, beta (dystrophin-associated glycoprotein)	0,63	0,0086
1453078_at	2610002M06Rik	RIKEN cDNA 2610002M06 gene	0,63	0,0394
1435115_at	Fndc5	fibronectin type III domain containing 5	0,63	0,0212
1436324_at	Stard9	START domain containing 9	0,63	0,0499
1460352_s_at	Pik3r4	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 4, p150	0,63	0,0049
1453646_at	3110005L21Rik	RIKEN cDNA 3110005L21 gene	0,63	0,0363
1433581_at	1190002N15Rik	RIKEN cDNA 1190002N15 gene	0,63	0,0257
1439675_at	Ppara	peroxisome proliferator activated receptor alpha	0,63	0,0102
1421297_a_at	Cacna1c	calcium channel, voltage-dependent, L type, alpha 1C subunit	0,63	0,0312
1450626_at	Manba	mannosidase, beta A, lysosomal	0,63	0,0221
1457214_at	NA	NA	0,63	0,0436
1458295_at	Tmem79	transmembrane protein 79	0,64	0,0347
1433851_at	Ppp4r2	protein phosphatase 4, regulatory subunit 2	0,64	0,0168
1423314_s_at	Pde7a	phosphodiesterase 7A	0,64	0,0412
1434758_at	Crispld2	cysteine-rich secretory protein LCCL domain containing 2	0,64	0,0021
1436719_at	Slc35f1	solute carrier family 35, member F1	0,64	0,0108
1437119_at	Ern1	endoplasmic reticulum (ER) to nucleus signalling 1	0,64	0,0255
1434093_at	Lysmd4	LysM, putative peptidoglycan-binding, domain containing 4	0,64	0,0136
1440936_at	Serac1	serine active site containing 1	0,64	0,0041
1417577_at	Trpc3	transient receptor potential cation channel, subfamily C, member 3	0,64	0,0174
1437212_at	Zfp420	zinc finger protein 420	0,64	0,0214
1417094_at	Acot7	acyl-CoA thioesterase 7	0,64	0,0255

1455659_at	Tmcc1	transmembrane and coiled coil domains 1	0,64	0,0047
1433978_at	4930430F08Rik	RIKEN cDNA 4930430F08 gene	0,64	0,0128
1440052_at	NA	NA	0,64	0,0039
1452295_at	Pmepa1	prostate transmembrane protein, androgen induced 1	0,64	0,0088
1443779_s_at	Lcor	ligand dependent nuclear receptor corepressor	0,64	0,0214
1419714_at	Cd274	CD274 antigen	0,64	0,0418
1444318_at	Chchd7	coiled-coil-helix-coiled-coil-helix domain containing 7	0,64	0,0238
1449526_a_at	Gdpd3	glycerophosphodiester phosphodiesterase domain containing 3	0,64	0,0200
1429555_at	Cldnd1	claudin domain containing 1	0,64	0,0255
1435254_at	Plxnb1	plexin B1	0,65	0,0200
1419292_at	Htra3	HtrA serine peptidase 3	0,65	0,0422
1433761_at	Pde4dip	phosphodiesterase 4D interacting protein (myomegalin)	0,65	0,0105
1431980_a_at	As3mt	arsenic (+3 oxidation state) methyltransferase	0,65	0,0365
1453424_at	Fyco1	FYVE and coiled-coil domain containing 1	0,65	0,0324
1455491_at	Hnrnph3	heterogeneous nuclear ribonucleoprotein H3	0,65	0,0086
1428198_at	Adal	adenosine deaminase-like	0,65	0,0347
1435851_at	Lgi1	leucine-rich repeat LGI family, member 1	0,65	0,0477
1428100_at	Sfrs1	splicing factor, arginine/serine-rich 1 (ASF/SF2)	0,65	0,0280
1436767_at	Luc7l2	LUC7-like 2 (S. cerevisiae)	0,65	0,0136
1425677_a_at	Ank1	ankyrin 1, erythroid	0,65	0,0476
1436244_a_at	Tle2	transducin-like enhancer of split 2, homolog of Drosophila E(spl)	0,65	0,0144
1441128_at	NA	NA	0,65	0,0200
1427287_s_at	Itpr2	inositol 1,4,5-triphosphate receptor 2	0,65	0,0237
1421265_a_at	Rbm38	RNA binding motif protein 38	0,65	0,0048
1454728_s_at	Atp8a1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	0,65	0,0428
1428725_at	Pias2	protein inhibitor of activated STAT 2	0,65	0,0157
1417408_at	F3	coagulation factor III	0,65	0,0150
1457721_at	Ppara	peroxisome proliferator activated receptor alpha	0,65	0,0086
1445484_at	Cycs	cytochrome c, somatic	0,65	0,0393
1424531_a_at	Tcea3	transcription elongation factor A (SII), 3	0,65	0,0128
1452462_a_at	Banp	BTG3 associated nuclear protein	0,65	0,0200
1427322_at	Brwd1	bromodomain and WD repeat domain containing 1	0,65	0,0324
1425186_at	Lmbrd1	LMBR1 domain containing 1	0,65	0,0099
1423979_a_at	Slc25a29	solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), member 29	0,65	0,0078
1435801_at	Fktn	fukutin	0,66	0,0028
1442525_at	NA	NA	0,66	0,0196
1457571_at	Zfp68	zinc finger protein 68	0,66	0,0065
1458358_at	Pank2	pantothenate kinase 2 (Hallervorden-Spatz syndrome)	0,66	0,0430
1430348_at	2900019E01Rik	RIKEN cDNA 2900019E01 gene	0,66	0,0389
1428255_at	Luc7l	Luc7 homolog (S. cerevisiae)-like	0,66	0,0086
1455647_at	Ar	androgen receptor	0,66	0,0154
1434815_a_at	Mapkapk3	mitogen-activated protein kinase-activated protein kinase 3	0,66	0,0483
1416772_at	Cpt2	carnitine palmitoyltransferase 2	0,66	0,0147
1456930_at	Camsap1	calmodulin regulated spectrin-associated protein 1	0,66	0,0042
1427089_at	Ccnt2	cyclin T2	0,66	0,0144
1430154_at	Vps13a	vacuolar protein sorting 13A (yeast)	0,66	0,0171
1435271_at	Irf3	interferon regulatory factor 3	0,66	0,0078
1451735_at	Arfrp1	ADP-ribosylation factor related protein 1	0,66	0,0255
1425568_a_at	Tmem33	transmembrane protein 33	0,66	0,0493

1460399_at	Ccdc117	coiled-coil domain containing 117	0,66	0,0293
1455625_at	NA	NA	0,66	0,0299
1416383_a_at	Pcx	pyruvate carboxylase	0,66	0,0173
1450332_s_at	Fmo5	flavin containing monooxygenase 5	0,66	0,0248
1423953_at	Cdkal1	CDK5 regulatory subunit associated protein 1-like 1	0,66	0,0361
1454976_at	Sod2	superoxide dismutase 2, mitochondrial	0,67	0,0114
1417846_at	Ulk2	Unc-51 like kinase 2 (C. elegans)	0,67	0,0288
1423750_a_at	Sf1	splicing factor 1	0,67	0,0134
1441198_at	Zfp39	zinc finger protein 39	0,67	0,0252
1452685_at	0610009O20Rik	RIKEN cDNA 0610009O20 gene	0,67	0,0444
1452821_at	Tial1	Tia1 cytotoxic granule-associated RNA binding protein-like 1	0,67	0,0134
1455003_at	Thap1	THAP domain containing, apoptosis associated protein 1	0,67	0,0319
1455405_at	Pstpip2	proline-serine-threonine phosphatase-interacting protein 2	0,67	0,0476
1417635_at	Spa17	sperm autoantigenic protein 17	0,67	0,0422
1423549_at	Slc1a4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	0,67	0,0284
1450627_at	Ank	progressive ankylosis	0,67	0,0438
1458302_at	NA	NA	0,67	0,0368
1428474_at	Ppp3cb	protein phosphatase 3, catalytic subunit, beta isoform	0,67	0,0237
1437041_at	Sfrs18	splicing factor, arginine/serine-rich 18	0,67	0,0299
1459048_s_at	Zfp142	zinc finger protein 142	0,67	0,0113
1419171_at	Fam174a	family with sequence similarity 174, member A	0,67	0,0125
1459874_s_at	Mtmr4	myotubularin related protein 4	0,67	0,0216
1435326_at	Lpgat1	lysophosphatidylglycerol acyltransferase 1	0,67	0,0147
1435096_at	Ric8b	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)	0,67	0,0090
1451361_a_at	Pnpla7	patatin-like phospholipase domain containing 7	0,67	0,0221
1436939_at	Unc45b	unc-45 homolog B (C. elegans)	0,67	0,0019
1436278_at	NA	NA	0,67	0,0078
1443833_at	NA	NA	0,67	0,0128
1422168_a_at	Bdnf	brain derived neurotrophic factor	0,67	0,0428
1457802_at	B930012P20Rik	RIKEN cDNA B930012P20 gene	0,67	0,0444
1448671_at	Ube2e3	ubiquitin-conjugating enzyme E2E 3, UBC4/5 homolog (yeast)	0,67	0,0341
1436277_at	Rnf207	ring finger protein 207	0,67	0,0171
1417788_at	Sncg	synuclein, gamma	0,67	0,0428
1454621_s_at	Fam73b	family with sequence similarity 73, member B	0,67	0,0477
1457532_at	NA	NA	0,67	0,0237
1450934_at	Eif4a2	eukaryotic translation initiation factor 4A2	0,68	0,0476
1435333_at	1110007M04Rik	RIKEN cDNA 1110007M04 gene	0,68	0,0091
1447987_at	Letm2	leucine zipper-EF-hand containing transmembrane protein 2	0,68	0,0455
1455334_at	D330038O06Rik	RIKEN cDNA D330038O06 gene	0,68	0,0225
1416083_at	Zfand5	zinc finger, AN1-type domain 5	0,68	0,0499
1437051_at	Dffb	DNA fragmentation factor, beta subunit	0,68	0,0109
1448136_at	Enpp2	ectonucleotide pyrophosphatase/phosphodiesterase 2	0,68	0,0344
1416400_at	Pycrl	pyrroline-5-carboxylate reductase-like	0,68	0,0361
1453003_at	Sorl1	sortilin-related receptor, LDLR class A repeats-containing	0,68	0,0405
1436458_at	Sema6a	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	0,68	0,0351

1434073_at	Gprasp2	G protein-coupled receptor associated sorting protein 2	0,68	0,0065
1438188_x_at	Slc25a29	solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), member 29	0,68	0,0299
1435594_at	Atl2	atlastin GTPase 2	0,68	0,0184
1444908_at	Habp4	hyaluronic acid binding protein 4	0,68	0,0065
1460458_at	Crispld2	cysteine-rich secretory protein LCCL domain containing 2	0,68	0,0317
1451467_s_at	Gtpbp5	GTP binding protein 5	0,68	0,0410
1435248_a_at	Btaf1	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot1 homolog, S. cerevisiae)	0,68	0,0317
1441460_at	NA	NA	0,68	0,0406
1448546_at	Rassf3	Ras association (RalGDS/AF-6) domain family member 3	0,68	0,0173
1434962_x_at	Ccl27a	chemokine (C-C motif) ligand 27A	0,68	0,0468
1417294_at	Akr7a5	aldo-keto reductase family 7, member A5 (aflatoxin aldehyde reductase)	0,68	0,0169
1460204_at	Tec	cytoplasmic tyrosine kinase, Dscr28C related (Drosophila)	0,68	0,0122
1453233_s_at	Calr3	calreticulin 3	0,68	0,0245
1418150_at	Mtmr4	myotubularin related protein 4	0,68	0,0188
1431199_at	0610031G08Rik	RIKEN cDNA 0610031G08 gene	0,68	0,0238
1435299_at	Cdk7	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	0,68	0,0081
1453461_at	Fxc1	fractured callus expressed transcript 1	0,68	0,0350
1451169_at	Nomo1	nodal modulator 1	0,68	0,0055
1438296_at	C430010C01	hypothetical protein C430010C01	0,68	0,0081
1426861_at	Aftph	aftiphilin	0,68	0,0133
1426782_at	Gpr125	G protein-coupled receptor 125	0,68	0,0368
1449443_at	Decr1	2,4-dienoyl CoA reductase 1, mitochondrial	0,69	0,0389
1440636_at	NA	NA	0,69	0,0443
1423063_at	Dnmt3a	DNA methyltransferase 3A	0,69	0,0168
1427971_at	Cdc73	cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	0,69	0,0284
1423272_at	Polg	polymerase (DNA directed), gamma	0,69	0,0332
1438006_at	4933439F18Rik	RIKEN cDNA 4933439F18 gene	0,69	0,0076
1428656_at	Rnasen	ribonuclease III, nuclear	0,69	0,0086
1435230_at	Ankrd12	ankyrin repeat domain 12	0,69	0,0203
1460200_s_at	Lztfl1	leucine zipper transcription factor-like 1	0,69	0,0428
1429723_at	6330409N04Rik	RIKEN cDNA 6330409N04 gene	0,69	0,0196
1423980_at	Slc25a29	solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), member 29	0,69	0,0206
1435469_at	Qsox2	quiescin Q6 sulfhydryl oxidase 2	0,69	0,0438
1428603_at	LOC100036521	hypothetical gene LOC100036521	0,69	0,0145
1415909_at	Stip1	stress-induced phosphoprotein 1	0,69	0,0275
1420127_s_at	Ccpg1	cell cycle progression 1	0,69	0,0055
1455139_at	AI851716	expressed sequence AI851716	0,69	0,0134
1439848_at	Bves	blood vessel epicardial substance	0,69	0,0064
1445655_at	NA	NA	0,69	0,0303
1420113_s_at	2410022L05Rik	RIKEN cDNA 2410022L05 gene	0,69	0,0065
1447881_x_at	NA	NA	0,69	0,0241
1422452_at	Bag3	BCL2-associated athanogene 3	0,69	0,0114
1419278_at	Usp48	ubiquitin specific peptidase 48	0,69	0,0235

1458161_at	Kcnq1ot1	KCNQ1 overlapping transcript 1	0,69	0,0391
1416182_at	Apba3	amyloid beta (A4) precursor protein-binding, family A, member 3	0,69	0,0132
1419401_at	Asb13	ankyrin repeat and SOCS box-containing 13	0,69	0,0418
1418472_at	Aspa	aspartoacylase	0,69	0,0394
1450859_s_at	Ube2d3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	0,69	0,0499
1415894_at	Enpp2	ectonucleotide pyrophosphatase/phosphodiesterase 2	0,69	0,0086
1417661_at	Rdm1	RAD52 motif 1	0,69	0,0173
1427874_at	Rnf114	ring finger protein 114	0,69	0,0478
1441649_at	NA	NA	0,69	0,0196
1424786_s_at	Wdr45	WD repeat domain 45	0,69	0,0065
1424622_at	Hsf1	heat shock factor 1	0,70	0,0456
1427969_s_at	Zfp654	zinc finger protein 654	0,70	0,0041
1417255_at	Ift140	intraflagellar transport 140 homolog (Chlamydomonas)	0,70	0,0341
1419261_at	Acad8	acyl-Coenzyme A dehydrogenase family, member 8	0,70	0,0198
1424308_at	Slc24a3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	0,70	0,0469
1423741_at	Rbm10	RNA binding motif protein 10	0,70	0,0241
1458404_at	Ndufb8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8	0,70	0,0103
1456875_at	1810013L24Rik	RIKEN cDNA 1810013L24 gene	0,70	0,0352
1437818_at	9430016H08Rik	RIKEN cDNA 9430016H08 gene	0,70	0,0444
1422579_at	Hspe1	heat shock protein 1 (chaperonin 10)	0,70	0,0311
1435668_at	Fam120b	family with sequence similarity 120, member B	0,70	0,0250
1419188_s_at	Ccl27a	chemokine (C-C motif) ligand 27A	0,70	0,0284
1451279_at	Erc1	ELKS/RAB6-interacting/CAST family member 1	0,70	0,0048
1429429_s_at	Pcmtd1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	0,70	0,0065
1436079_s_at	Vapb	vesicle-associated membrane protein, associated protein B and C	0,70	0,0074
1428804_at	Mfap3l	microfibrillar-associated protein 3-like	0,70	0,0275
1453372_at	Dnajc1	DnaJ (Hsp40) homolog, subfamily C, member 1	0,70	0,0433
1439027_at	C330023M02Rik	RIKEN cDNA C330023M02 gene	0,70	0,0113
1455376_at	1300010F03Rik	RIKEN cDNA 1300010F03 gene	0,70	0,0249
1432901_at	Etl4	enhancer trap locus 4	0,70	0,0273
1455320_at	NA	NA	0,70	0,0341
1453485_s_at	1110005A03Rik	RIKEN cDNA 1110005A03 gene	0,70	0,0138
1436143_at	Nbas	neuroblastoma amplified sequence	0,70	0,0283
1440769_at	2010305A19Rik	RIKEN cDNA 2010305A19 gene	0,70	0,0059
1418743_a_at	Tesc	tescalcin	0,70	0,0443
1434999_at	Suv420h1	suppressor of variegation 4-20 homolog 1 (Drosophila)	0,70	0,0174
1434267_at	Nek1	NIMA (never in mitosis gene a)-related expressed kinase 1	0,70	0,0146
1428614_at	Ldhd	lactate dehydrogenase D	0,70	0,0047
1425210_s_at	Zfp84	zinc finger protein 84	0,70	0,0171
1452005_at	Dlat	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	0,70	0,0298
1436560_at	Kif3a	kinesin family member 3A	0,70	0,0428
1449501_a_at	Gzmm	granzyme M (lymphocyte met-ase 1)	0,70	0,0442
1417008_at	Crat	carnitine acetyltransferase	0,70	0,0049
1438415_s_at	Yipf2	Yip1 domain family, member 2	0,70	0,0499

1434161_at	Lin52	lin-52 homolog (C. elegans)	0,70	0,0279
1417190_at	Nampt	nicotinamide phosphoribosyltransferase	0,70	0,0341
1437300_at	Mef2d	myocyte enhancer factor 2D	0,70	0,0379
1428978_at	2900009J20Rik	RIKEN cDNA 2900009J20 gene	0,70	0,0229
1422482_at	Ruvbl2	RuvB-like protein 2	0,70	0,0168
1450204_a_at	Mynn	myoneurin	0,70	0,0235
1456981_at	Tmc7	transmembrane channel-like gene family 7	0,71	0,0426
1449459_s_at	Asb13	ankyrin repeat and SOCS box-containing 13	0,71	0,0203
1415743_at	Hdac5	histone deacetylase 5	0,71	0,0367
1423981_x_at	Slc25a29	solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), member 29	0,71	0,0169
1436641_at	AI415730	expressed sequence AI415730	0,71	0,0426
1439509_at	2900008C10Rik	RIKEN cDNA 2900008C10 gene	0,71	0,0055
1440345_at	AI450353	expressed sequence AI450353	0,71	0,0361
1455094_s_at	Ube2g1	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans)	0,71	0,0078
1417791_a_at	Zfml	zinc finger, matrin-like	0,71	0,0370
1458425_at	NA	NA	0,71	0,0081
1419646_a_at	Mbp	myelin basic protein	0,71	0,0461
1460676_at	Josd1	Josephin domain containing 1	0,71	0,0293
1424480_s_at	Akt2	thymoma viral proto-oncogene 2	0,71	0,0102
1427469_at	Helz	helicase with zinc finger domain	0,71	0,0186
1433737_at	Uhmk1	U2AF homology motif (UHM) kinase 1	0,71	0,0368
1445492_at	NA	NA	0,71	0,0287
1439895_at	AU021025	expressed sequence AU021025	0,71	0,0103
1435066_at	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	0,71	0,0184
1423074_at	Lman2	lectin, mannose-binding 2	0,71	0,0422
1437056_x_at	Crispld2	cysteine-rich secretory protein LCCL domain containing 2	0,71	0,0290
1456753_at	NA	NA	0,71	0,0153
1459665_s_at	Mrvi1	MRV integration site 1	0,71	0,0164
1426840_at	Ythdf3	YTH domain family 3	0,71	0,0129
1434307_at	Tmem64	transmembrane protein 64	0,71	0,0341
1439103_at	Cdc73	cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	0,71	0,0339
1460082_at	Ing3	inhibitor of growth family, member 3	0,71	0,0103
1419477_at	Clec2d	C-type lectin domain family 2, member d	0,71	0,0283
1424391_at	Nrd1	nardilysin, N-arginine dibasic convertase, NRD convertase 1	0,71	0,0048
1441551_at	Mypn	myopalladin	0,71	0,0209
1417857_at	Mmaa	methylmalonic aciduria (cobalamin deficiency) type A	0,71	0,0339
1447547_at	Ltbp1	latent transforming growth factor beta binding protein 1	0,71	0,0078
1426351_at	Hspd1	heat shock protein 1 (chaperonin)	0,71	0,0230
1433901_at	Caprin1	cell cycle associated protein 1	0,71	0,0449
1436072_at	Zfp826	zinc finger protein 826	0,71	0,0177
1436555_at	Slc7a2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	0,71	0,0475
1453350_at	2010005J08Rik	RIKEN cDNA 2010005J08 gene	0,72	0,0325
1440856_at	Mapk8	mitogen-activated protein kinase 8	0,72	0,0062
1419824_a_at	Aasdh	aminoadipate-semialdehyde dehydrogenase	0,72	0,0341
1429715_at	Ppp2r2a	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	0,72	0,0142
1434781_at	Dnajc16	DnaJ (Hsp40) homolog, subfamily C, member 16	0,72	0,0368
1432916_at	5730407I0	RIKEN cDNA 5730407I07 gene	0,72	0,0382

	7Rik			
1454891_at	Cds2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	0,72	0,0428
1437364_at	Coq3	coenzyme Q3 homolog, methyltransferase (yeast)	0,72	0,0357
1455850_at	2310003H01Rik	RIKEN cDNA 2310003H01 gene	0,72	0,0491
1449075_at	Exdl2	exonuclease 3"-5" domain-like 2	0,72	0,0484
1454796_at	Ficd	FIC domain containing	0,72	0,0340
1424420_at	Ccpg1	cell cycle progression 1	0,72	0,0093
1434511_at	Phkb	phosphorylase kinase beta	0,72	0,0422
1417003_at	0610012G03Rik	RIKEN cDNA 0610012G03 gene	0,72	0,0375
1428696_at	Rftn1	raftlin lipid raft linker 1	0,72	0,0341
1433860_at	6030458C11Rik	RIKEN cDNA 6030458C11 gene	0,72	0,0180
1451729_at	Bmpr1a	bone morphogenetic protein receptor, type 1A	0,72	0,0153
1425037_at	Fgd4	FYVE, RhoGEF and PH domain containing 4	0,72	0,0291
1424323_at	Noc2l	nucleolar complex associated 2 homolog (S. cerevisiae)	0,72	0,0212
1419455_at	Il10rb	interleukin 10 receptor, beta	0,72	0,0379
1434150_a_at	Mettl7a1	methyltransferase like 7A1	0,72	0,0499
1435700_at	Tln2	talin 2	0,72	0,0238
1418308_at	Hus1	Hus1 homolog (S. pombe)	0,72	0,0255
1459765_s_at	Sf1	splicing factor 1	0,72	0,0230
1429396_at	Atg16l2	autophagy related 16 like 2 (S. cerevisiae)	0,72	0,0376
1434051_s_at	Hspa12a	heat shock protein 12A	0,72	0,0499
1415689_s_at	Zkscan3	zinc finger with KRAB and SCAN domains 3	0,72	0,0499
1457811_at	NA	NA	0,72	0,0203
1455597_at	Map3k2	mitogen-activated protein kinase kinase kinase 2	0,72	0,0059
1452687_at	Dus2l	dihydrouridine synthase 2-like (SMM1, S. cerevisiae)	0,72	0,0047
1415812_at	Gsn	gelsolin	0,72	0,0159
1418706_at	Slc38a3	solute carrier family 38, member 3	0,72	0,0293
1425508_s_at	Arfrp1	ADP-ribosylation factor related protein 1	0,72	0,0340
1426584_a_at	Sord	sorbitol dehydrogenase	0,72	0,0164
1443992_at	Nipbl	Nipped-B homolog (Drosophila)	0,72	0,0227
1416775_at	Atp5sl	ATP5S-like	0,72	0,0237
1429064_at	Dip2c	DIP2 disco-interacting protein 2 homolog C (Drosophila)	0,72	0,0028
1422895_at	Vamp4	vesicle-associated membrane protein 4	0,73	0,0341
1423068_at	Ift172	intraflagellar transport 172 homolog (Chlamydomonas)	0,73	0,0111
1423351_at	Mrpl1	mitochondrial ribosomal protein L1	0,73	0,0448
1442348_at	NA	NA	0,73	0,0230
1416275_at	Slc26a6	solute carrier family 26, member 6	0,73	0,0418
1451422_at	Myo18a	myosin XVIIIA	0,73	0,0484
1435905_at	D3Ertd300e	DNA segment, Chr 3, ERATO Doi 300, expressed	0,73	0,0041
1438533_at	Myo9b	myosin IXb	0,73	0,0298
1444550_at	1110021J02Rik	RIKEN cDNA 1110021J02 gene	0,73	0,0088
1440384_at	Tmcc1	transmembrane and coiled coil domains 1	0,73	0,0065
1436315_at	Myst3	MYST histone acetyltransferase (monocytic leukemia) 3	0,73	0,0203
1428403_at	2410025L10Rik	RIKEN cDNA 2410025L10 gene	0,73	0,0083
1451523_a_at	Mif4gd	MIF4G domain containing	0,73	0,0132
1452047_at	Cacybp	calcyclin binding protein	0,73	0,0416
1440003_at	NA	NA	0,73	0,0384

1455412_at	Sfmbt1	Scm-like with four mbt domains 1	0,73	0,0299
1455656_at	Btla	B and T lymphocyte associated	0,73	0,0426
1415684_at	Atg5	autophagy-related 5 (yeast)	0,73	0,0392
1452942_at	Tmem65	transmembrane protein 65	0,73	0,0170
1424223_at	1700020C11Rik	RIKEN cDNA 1700020C11 gene	0,73	0,0157
1416752_at	Ldb3	LIM domain binding 3	0,73	0,0214
1433942_at	Myo6	myosin VI	0,73	0,0174
1429819_at	Nmnat1	nicotinamide nucleotide adenylyltransferase 1	0,73	0,0113
1429017_at	Smcr8	Smith-Magenis syndrome chromosome region, candidate 8 homolog (human)	0,73	0,0109
1418694_at	Kcmf1	potassium channel modulatory factor 1	0,73	0,0456
1437382_at	Acvr2a	activin receptor IIA	0,73	0,0168
1455538_at	6330403M23Rik	RIKEN cDNA 6330403M23 gene	0,73	0,0499
1449333_at	Sf3a1	splicing factor 3a, subunit 1	0,73	0,0171
1429115_at	2010003O02Rik	RIKEN cDNA 2010003O02 gene	0,73	0,0173
1454988_s_at	Rab22a	RAB22A, member RAS oncogene family	0,73	0,0206
1420641_a_at	Sqrdl	sulfide quinone reductase-like (yeast)	0,73	0,0157
AFFX-PyruCarbMur/L09192_3_at	Pcx	pyruvate carboxylase	0,73	0,0196
1416364_at	Hsp90ab1	heat shock protein 90 alpha (cytosolic), class B member 1	0,73	0,0086
1451573_a_at	Stx4a	syntaxin 4A (placental)	0,73	0,0222
1426353_at	Stat6	signal transducer and activator of transcription 6	0,73	0,0480
1451448_a_at	1110005A03Rik	RIKEN cDNA 1110005A03 gene	0,73	0,0103
1417152_at	Nacc2	nucleus accumbens associated 2, BEN and BTB (POZ) domain containing	0,73	0,0155
1428651_at	Klhl24	kelch-like 24 (Drosophila)	0,73	0,0316
1421867_at	Nr3c1	nuclear receptor subfamily 3, group C, member 1	0,73	0,0436
1423106_at	Ube2b	ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae)	0,73	0,0360
1427406_at	Trip11	thyroid hormone receptor interactor 11	0,74	0,0273
1448717_at	Gcdh	glutaryl-Coenzyme A dehydrogenase	0,74	0,0238
1453036_at	5430439M09Rik	RIKEN cDNA 5430439M09 gene	0,74	0,0113
1450058_at	Asph	aspartate-beta-hydroxylase	0,74	0,0146
1449019_at	Akap1	A kinase (PRKA) anchor protein 1	0,74	0,0021
1417568_at	Ncald	neurocalcin delta	0,74	0,0344
1428755_at	Creb1	cAMP responsive element binding protein 1	0,74	0,0375
1427091_at	Znfx1	zinc finger, NFX1-type containing 1	0,74	0,0235
1457673_at	6820431F20Rik	RIKEN cDNA 6820431F20 gene	0,74	0,0361
1418578_at	Dgka	diacylglycerol kinase, alpha	0,74	0,0232
1420776_a_at	Auh	AU RNA binding protein/enoyl-coenzyme A hydratase	0,74	0,0047
1435074_at	Tmem106b	transmembrane protein 106B	0,74	0,0109
1455817_x_at	Zxdb	zinc finger, X-linked, duplicated B	0,74	0,0203
1457059_at	Zfp438	zinc finger protein 438	0,74	0,0426
1437230_at	Kcna1	potassium voltage-gated channel, shaker-related subfamily, member 1	0,74	0,0443
1438315_x_at	Akr7a5	aldo-keto reductase family 7, member A5 (aflatoxin aldehyde reductase)	0,74	0,0200
1417505_s_at	Il11ra1	interleukin 11 receptor, alpha chain 1	0,74	0,0041
1448835_at	E2f6	E2F transcription factor 6	0,74	0,0196
1452110_at	Mtrr	5-methyltetrahydrofolate-homocysteine	0,74	0,0391

		methyltransferase reductase		
1451801_at	Trdn	triadin	0,74	0,0325
1460687_at	Setd8	SET domain containing (lysine methyltransferase) 8	0,74	0,0341
1446528_at	Scyl2	SCY1-like 2 (S. cerevisiae)	0,74	0,0438
1434168_at	Peo1	progressive external ophthalmoplegia 1 (human)	0,74	0,0048
1447961_s_at	Mrpl38	mitochondrial ribosomal protein L38	0,74	0,0350
1452727_at	R3hdm2	R3H domain containing 2	0,74	0,0486
1451274_at	Ogdh	oxoglutarate dehydrogenase (lipoamide)	0,74	0,0102
1417516_at	Ddit3	DNA-damage inducible transcript 3	0,74	0,0348
1435797_at	D5Wsu178e	DNA segment, Chr 5, Wayne State University 178, expressed	0,74	0,0303
1417375_at	Tuba4a	tubulin, alpha 4A	0,74	0,0361
1417305_at	Speg	SPEG complex locus	0,74	0,0153
1457709_a_at	A930005H10Rik	RIKEN cDNA A930005H10 gene	0,74	0,0416
1448733_at	Bmi1	Bmi1 polycomb ring finger oncogene	0,74	0,0131
1460631_at	Ogt	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	0,74	0,0150
1438838_at	B230206F22Rik	RIKEN cDNA B230206F22 gene	0,74	0,0303
1435489_at	NA	NA	0,74	0,0299
1416170_at	Trap1	TNF receptor-associated protein 1	0,74	0,0341
1425372_at	Dnajc19	DnaJ (Hsp40) homolog, subfamily C, member 19	0,74	0,0288
1448645_at	Msl3	male-specific lethal 3 homolog (Drosophila)	0,74	0,0203
1451539_at	Baiap2l1	BAI1-associated protein 2-like 1	0,74	0,0227
1418529_at	Osgep	O-sialoglycoprotein endopeptidase	0,74	0,0079
1439278_at	Zbtb20	zinc finger and BTB domain containing 20	0,75	0,0055
1426780_at	D14Ertd436e	DNA segment, Chr 14, ERATO Doi 436, expressed	0,75	0,0303
1416859_at	Fkbp3	FK506 binding protein 3	0,75	0,0410
1435004_at	Pank4	pantothenate kinase 4	0,75	0,0274
1427052_at	Acacb	acetyl-Coenzyme A carboxylase beta	0,75	0,0217
1452331_s_at	Qser1	glutamine and serine rich 1	0,75	0,0369
1438022_at	Rab11fip3	RAB11 family interacting protein 3 (class II)	0,75	0,0164
1415920_at	Cstf2t	cleavage stimulation factor, 3' pre-RNA subunit 2, tau	0,75	0,0147
1434266_at	AI847670	expressed sequence AI847670	0,75	0,0499
1438409_at	Cep63	centrosomal protein 63	0,75	0,0059
1415986_at	Clcn4-2	chloride channel 4-2	0,75	0,0053
1435251_at	Snx13	sorting nexin 13	0,75	0,0303
1430421_a_at	Tmem205	transmembrane protein 205	0,75	0,0300
1451745_a_at	Znhit1	zinc finger, HIT domain containing 1	0,75	0,0264
1441481_at	Mfap3l	microfibrillar-associated protein 3-like	0,75	0,0351
1419122_at	Mettl1	methyltransferase like 1	0,75	0,0413
1436597_at	Ankhd1	ankyrin repeat and KH domain containing 1	0,75	0,0308
1417908_s_at	Ube2l3	ubiquitin-conjugating enzyme E2L 3	0,75	0,0443
1443979_at	A830021K08Rik	RIKEN cDNA A830021K08 gene	0,75	0,0168
1438008_at	Gga3	golgi associated, gamma adaptin ear containing, ARF binding protein 3	0,75	0,0238
1456312_x_at	Gsn	gelsolin	0,75	0,0078
1449575_a_at	Gstp1	glutathione S-transferase, pi 1	0,75	0,0028
1424418_at	Slc25a38	solute carrier family 25, member 38	0,75	0,0330
1415715_at	Tmem129	transmembrane protein 129	0,75	0,0308
1424205_at	Smarca5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	0,75	0,0391
1455227_at	Aadacl1	arylacetamide deacetylase-like 1	0,75	0,0141

1437350_at	Dph1	DPH1 homolog (S. cerevisiae)	0,75	0,0351
1426984_at	2310067B10Rik	RIKEN cDNA 2310067B10 gene	0,75	0,0081
1422612_at	Hk2	hexokinase 2	0,75	0,0210
1438317_a_at	D2Wsu81e	DNA segment, Chr 2, Wayne State University 81, expressed	0,75	0,0447
1457285_at	Zfp187	zinc finger protein 187	0,75	0,0303
1419428_a_at	Gaa	glucosidase, alpha, acid	0,75	0,0298
1453311_at	2310008B10Rik	RIKEN cDNA 2310008B10 gene	0,75	0,0368
1424166_at	Msh3	mutS homolog 3 (E. coli)	0,75	0,0203
1437875_at	Bicd2	bicaudal D homolog 2 (Drosophila)	0,75	0,0324
1456763_at	Mprip	myosin phosphatase Rho interacting protein	0,75	0,0293
1451754_a_at	Wdr45	WD repeat domain 45	0,75	0,0138
1452053_a_at	Tmem33	transmembrane protein 33	0,75	0,0196
1428293_at	2310022M17Rik	RIKEN cDNA 2310022M17 gene	0,75	0,0223
1456013_x_at	Slc35a4	solute carrier family 35, member A4	0,75	0,0381
1436113_a_at	St13	suppression of tumorigenicity 13	0,75	0,0220
1447784_x_at	Slc38a9	solute carrier family 38, member 9	0,75	0,0442
1437171_x_at	Gsn	gelsolin	0,76	0,0086
1423663_at	Flcn	folliculin	0,76	0,0449
1448096_at	Ogfod1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	0,76	0,0422
1449608_a_at	NA	NA	0,76	0,0273
1429767_at	2810013P06Rik	RIKEN cDNA 2810013P06 gene	0,76	0,0274
1449150_at	Krba1	KRAB-A domain containing 1	0,76	0,0391
1434551_at	Hnrnpul2	heterogeneous nuclear ribonucleoprotein U-like 2	0,76	0,0279
1434870_at	2810004N23Rik	RIKEN cDNA 2810004N23 gene	0,76	0,0186
1458527_at	NA	NA	0,76	0,0249
1424103_at	Atg4b	autophagy-related 4B (yeast)	0,76	0,0128
1422524_at	Abcb6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	0,76	0,0496
1428502_at	Actr6	ARP6 actin-related protein 6 homolog (yeast)	0,76	0,0394
1427191_at	Npr2	natriuretic peptide receptor 2	0,76	0,0449
1437379_x_at	Trap1	TNF receptor-associated protein 1	0,76	0,0117
1434151_at	Mettl7a1	methyltransferase like 7A1	0,76	0,0194
1452105_a_at	Tsc2	tuberous sclerosis 2	0,76	0,0153
1427045_at	Synpo	synaptopodin	0,76	0,0464
1424052_at	Thap4	THAP domain containing 4	0,76	0,0173
1435464_at	1110003E01Rik	RIKEN cDNA 1110003E01 gene	0,76	0,0128
1453782_at	3021401C12Rik	RIKEN cDNA 3021401C12 gene	0,76	0,0436
1451556_a_at	2700078E11Rik	RIKEN cDNA 2700078E11 gene	0,76	0,0442
1455734_at	Crbn	cereblon	0,76	0,0456
1418593_at	Taf6	TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor	0,76	0,0477
1452996_a_at	Aven	apoptosis, caspase activation inhibitor	0,76	0,0443
1426624_a_at	Ypel3	yippee-like 3 (Drosophila)	0,76	0,0375
1423575_a_at	Wbscr22	Williams Beuren syndrome chromosome region 22	0,76	0,0461
1416522_a_at	Grcc10	gene rich cluster, C10 gene	0,76	0,0102
1451525_at	Arhgap12	Rho GTPase activating protein 12	0,76	0,0373
1454406_at	4930453J04Rik	RIKEN cDNA 4930453J04 gene	0,77	0,0081

1429315_at	Syt11	synaptotagmin XI	0,77	0,0180
1427014_at	Dennd4b	DENN/MADD domain containing 4B	0,77	0,0275
1435171_at	2810416G20Rik	RIKEN cDNA 2810416G20 gene	0,77	0,0422
1422797_at	Robld3	roadblock domain containing 3	0,77	0,0253
1448971_at	2410022L05Rik	RIKEN cDNA 2410022L05 gene	0,77	0,0319
1421962_at	Dnajb5	DnaJ (Hsp40) homolog, subfamily B, member 5	0,77	0,0361
1429539_at	Bcl2l13	BCL2-like 13 (apoptosis facilitator)	0,77	0,0214
1426041_a_at	Fgd4	FYVE, RhoGEF and PH domain containing 4	0,77	0,0391
1435841_s_at	Suclg2	succinate-Coenzyme A ligase, GDP-forming, beta subunit	0,77	0,0173
1458339_at	Cdadc1	cytidine and dCMP deaminase domain containing 1	0,77	0,0442
1452877_at	2700029M09Rik	RIKEN cDNA 2700029M09 gene	0,77	0,0385
1423229_at	Inpp5e	inositol polyphosphate-5-phosphatase E	0,77	0,0184
1435813_at	Mypn	myopalladin	0,77	0,0203
1426445_at	Ctage5	CTAGE family, member 5	0,77	0,0218
1455187_at	Zbtb40	zinc finger and BTB domain containing 40	0,77	0,0390
1435443_at	Eya3	eyes absent 3 homolog (Drosophila)	0,77	0,0440
1437494_at	Mapkapk3	mitogen-activated protein kinase-activated protein kinase 3	0,77	0,0410
1425975_a_at	Mapk8ip3	mitogen-activated protein kinase 8 interacting protein 3	0,77	0,0169
1418793_at	Idua	iduronidase, alpha-L-	0,77	0,0295
1417142_at	Fam120b	family with sequence similarity 120, member B	0,77	0,0210
1450884_at	Cd36	CD36 antigen	0,77	0,0196
1455747_at	Ggt5	gamma-glutamyltransferase 5	0,77	0,0476
1417221_at	Ppm1a	protein phosphatase 1A, magnesium dependent, alpha isoform	0,77	0,0355
1435733_x_at	Rnaseh2c	ribonuclease H2, subunit C	0,77	0,0443
1433586_at	Rgmb	RGM domain family, member B	0,77	0,0283
1430107_at	Acbd7	acyl-Coenzyme A binding domain containing 7	0,77	0,0495
1433514_at	Etnk1	ethanolamine kinase 1	0,77	0,0496
1427407_s_at	Trip11	thyroid hormone receptor interactor 11	0,77	0,0422
1419380_at	Zfp423	zinc finger protein 423	0,77	0,0499
1418222_at	2610024G14Rik	RIKEN cDNA 2610024G14 gene	0,77	0,0428
1435417_at	AI464131	expressed sequence AI464131	0,77	0,0180
1451264_at	Frmd6	FERM domain containing 6	0,77	0,0443
1436991_x_at	Gsn	gelsolin	0,77	0,0147
1434710_at	Dhx29	DEAH (Asp-Glu-Ala-His) box polypeptide 29	0,77	0,0214
1419835_s_at	Plec1	plectin 1	0,77	0,0406
1417088_at	Zfp346	zinc finger protein 346	0,77	0,0342
1453230_at	Zfp74	zinc finger protein 74	0,77	0,0411
1425492_at	Bmpr1a	bone morphogenetic protein receptor, type 1A	0,77	0,0422
1454873_at	Zfp775	zinc finger protein 775	0,77	0,0330
1435787_at	Ppm1l	protein phosphatase 1 (formerly 2C)-like	0,77	0,0398
1416513_at	Lamb2	laminin, beta 2	0,77	0,0443
1429598_at	2310042D19Rik	RIKEN cDNA 2310042D19 gene	0,77	0,0138
1415691_at	Dlg1	discs, large homolog 1 (Drosophila)	0,77	0,0430
1435836_at	Pdk1	pyruvate dehydrogenase kinase, isoenzyme 1	0,77	0,0235
1433799_at	Rdh13	retinol dehydrogenase 13 (all-trans and 9-cis)	0,77	0,0456
1455450_at	Ptpn3	protein tyrosine phosphatase, non-receptor type 3	0,77	0,0284
1424076_at	Gdpd1	glycerophosphodiester phosphodiesterase domain containing 1	0,78	0,0481
1420630_at	8430419L0	RIKEN cDNA 8430419L09 gene	0,78	0,0444

	9Rik			
1423925_at	Dhx16	DEAH (Asp-Glu-Ala-His) box polypeptide 16	0,78	0,0238
1427342_at	Fastkd1	FAST kinase domains 1	0,78	0,0390
1424054_at	Btbd2	BTB (POZ) domain containing 2	0,78	0,0337
1426583_at	Atf2	activating transcription factor 2	0,78	0,0128
1453097_a_at	Ubtf	upstream binding transcription factor, RNA polymerase I	0,78	0,0105
1427917_s_at	Ssbp3	single-stranded DNA binding protein 3	0,78	0,0086
1427887_at	Rprd1b	regulation of nuclear pre-mRNA domain containing 1B	0,78	0,0190
1421469_a_at	Stat5a	signal transducer and activator of transcription 5A	0,78	0,0433
1423360_at	Yme1l1	YME1-like 1 (S. cerevisiae)	0,78	0,0430
1418463_at	Pik3r2	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 beta)	0,78	0,0365
1429748_at	Qk	quaking	0,78	0,0127
1455244_at	Daam1	dishevelled associated activator of morphogenesis 1	0,78	0,0443
1420510_at	Srfbp1	serum response factor binding protein 1	0,78	0,0303
1448900_at	D16H22S680E	DNA segment, Chr 16, human D22S680E, expressed	0,78	0,0358
1451970_at	Daglb	diacylglycerol lipase, beta	0,78	0,0299
1435684_at	Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	0,78	0,0308
1459640_at	NA	NA	0,78	0,0147
1443890_at	NA	NA	0,78	0,0167
1451980_at	Casd1	CAS1 domain containing 1	0,78	0,0308
1415714_a_at	Snrnp27	small nuclear ribonucleoprotein 27 (U4/U6.U5)	0,78	0,0260
1435752_s_at	Abcc9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	0,78	0,0347
1434190_at	Sms	spermine synthase	0,78	0,0128
1452637_a_at	Bola1	bolA-like 1 (E. coli)	0,78	0,0128
1457245_at	Dirc2	disrupted in renal carcinoma 2 (human)	0,78	0,0279
1423958_a_at	Ttc33	tetratricopeptide repeat domain 33	0,79	0,0099
1415949_at	Cpe	carboxypeptidase E	0,79	0,0136
1435538_at	0610030E20Rik	RIKEN cDNA 0610030E20 gene	0,79	0,0326
1418342_at	Rfc1	replication factor C (activator 1) 1	0,79	0,0443
1428613_at	Ldhd	lactate dehydrogenase D	0,79	0,0241
1459868_x_at	100038993	predicted gene, 100038993	0,79	0,0185
1421052_a_at	Sms	spermine synthase	0,79	0,0231
1423613_at	Ssfa2	sperm specific antigen 2	0,79	0,0371
1451677_at	Narf	nuclear prelamin A recognition factor	0,79	0,0387
1416616_s_at	Clpp	caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli)	0,79	0,0284
1452791_at	Coq2	coenzyme Q2 homolog, prenyltransferase (yeast)	0,79	0,0109
1428365_a_at	Lonp1	lon peptidase 1, mitochondrial	0,79	0,0172
1449097_at	Txnrd2	thioredoxin reductase 2	0,79	0,0167
1435867_at	Jhdm1d	jumonji C domain-containing histone demethylase 1 homolog D (S. cerevisiae)	0,79	0,0139
1460252_s_at	Zfp105	zinc finger protein 105	0,79	0,0348
1449003_a_at	Vti1b	vesicle transport through interaction with t-SNAREs 1B homolog	0,79	0,0113
1457826_a_at	1810043H04Rik	RIKEN cDNA 1810043H04 gene	0,79	0,0470
1435025_at	Ogfod1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	0,79	0,0432
1456072_at	Ppp1r9a	protein phosphatase 1, regulatory (inhibitor) subunit 9A	0,79	0,0365
1424006_at	Aarsd1	alanyl-tRNA synthetase domain containing 1	0,79	0,0428
1417247_at	AI597479	expressed sequence AI597479	0,79	0,0194

1452943_at	Tmem65	transmembrane protein 65	0,79	0,0391
1455434_a_at	Ktn1	kinectin 1	0,79	0,0152
1458721_at	Pcdhg@	protocadherin gamma cluster	0,79	0,0238
1418347_at	Ccdc22	coiled-coil domain containing 22	0,79	0,0375
1438695_at	C230091D08Rik	RIKEN cDNA C230091D08 gene	0,79	0,0215
1435878_at	Stk38l	serine/threonine kinase 38 like	0,79	0,0155
1457801_at	9930024M15Rik	RIKEN cDNA 9930024M15 gene	0,79	0,0449
1423044_at	Prosc	proline synthetase co-transcribed	0,79	0,0246
1433875_at	4732418C07Rik	RIKEN cDNA 4732418C07 gene	0,79	0,0189
1423532_at	Rnf44	ring finger protein 44	0,80	0,0297
1424377_at	BC003885	cDNA sequence BC003885	0,80	0,0326
1451170_s_at	Nomo1	nodal modulator 1	0,80	0,0428
1441919_x_at	Crat	carnitine acetyltransferase	0,80	0,0287
1434179_at	Mll3	myeloid/lymphoid or mixed-lineage leukemia 3	0,80	0,0303
1427274_at	Rnf214	ring finger protein 214	0,80	0,0139
1424282_at	Pet112l	PET112-like (yeast)	0,80	0,0252
1455621_at	BC066107	cDNA sequence BC066107	0,80	0,0161
1416655_at	C1galt1c1	C1GALT1-specific chaperone 1	0,80	0,0444
1455829_at	Usp14	ubiquitin specific peptidase 14	0,80	0,0410
1424949_at	Huwe1	HECT, UBA and WWE domain containing 1	0,80	0,0348
1433669_at	Akap8	A kinase (PRKA) anchor protein 8	0,80	0,0213
1454902_at	Prkcz	protein kinase C, zeta	0,80	0,0391
1430417_s_at	Neurl4	neuralized homolog 4 (Drosophila)	0,80	0,0348
1441192_at	Scly	selenocysteine lyase	0,80	0,0355
1425773_s_at	Nmnat1	nicotinamide nucleotide adenylyltransferase 1	0,80	0,0499
1422103_a_at	Stat5b	signal transducer and activator of transcription 5B	0,80	0,0413
1444998_at	NA	NA	0,80	0,0172
1419687_at	Macrod1	MACRO domain containing 1	0,80	0,0215
1417964_at	Ap3d1	adaptor-related protein complex 3, delta 1 subunit	0,81	0,0330
1450690_at	Ranbp2	RAN binding protein 2	0,81	0,0293
1460548_a_at	Eral1	Era (G-protein)-like 1 (E. coli)	0,81	0,0444
1448247_at	Bcl7b	B-cell CLL/lymphoma 7B	0,81	0,0140
1444774_at	Det1	de-etiolated homolog 1 (Arabidopsis)	0,81	0,0462
1455481_at	Ids	iduronate 2-sulfatase	0,81	0,0134
1416224_at	Zbtb17	zinc finger and BTB domain containing 17	0,81	0,0217
1427446_s_at	Ttn	titin	0,81	0,0277
1442752_at	NA	NA	0,81	0,0215
1424336_at	Ppcdc	phosphopantothenoylcysteine decarboxylase	0,81	0,0452
1460446_at	Wrb	tryptophan rich basic protein	0,81	0,0375
1428821_at	Agpat2	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	0,81	0,0473
1428411_at	1700020I14Rik	RIKEN cDNA 1700020I14 gene	0,81	0,0373
1416534_at	Dpf2	D4, zinc and double PHD fingers family 2	0,81	0,0106
1424368_s_at	Ubqln1	ubiquilin 1	0,81	0,0290
1433497_at	Aqr	aquarius	0,81	0,0171
1451665_a_at	Ap4s1	adaptor-related protein complex AP-4, sigma 1	0,81	0,0361
1453685_at	Nudt7	nudix (nucleoside diphosphate linked moiety X)-type motif 7	0,81	0,0373
1452116_s_at	Atf2	activating transcription factor 2	0,81	0,0451
1452773_at	5730494N06Rik	RIKEN cDNA 5730494N06 gene	0,82	0,0499
1423785_at	Egln1	EGL nine homolog 1 (C. elegans)	0,82	0,0131

1423534_at	Pdcd2	programmed cell death 2	0,82	0,0278
1435501_at	Atg2b	ATG2 autophagy related 2 homolog B (S. cerevisiae)	0,82	0,0394
1454657_s_at	Mak10	MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)	0,82	0,0355
1454982_at	Arfgef2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	0,82	0,0284
1417674_s_at	Golga4	golgi autoantigen, golgin subfamily a, 4	0,82	0,0158
1456569_x_at	Gsn	gelsolin	0,82	0,0341
1426760_at	Ipo8	importin 8	0,82	0,0368
1452052_s_at	Eif3j	eukaryotic translation initiation factor 3, subunit J	0,82	0,0298
1426382_at	Ppm1b	protein phosphatase 1B, magnesium dependent, beta isoform	0,82	0,0291
1417099_at	Ftsj1	FtsJ homolog 1 (E. coli)	0,82	0,0499
1453518_at	Pdzd11	PDZ domain containing 11	0,82	0,0448
1423690_s_at	Gpsm1	G-protein signalling modulator 1 (AGS3-like, C. elegans)	0,82	0,0256
1428473_at	Ppp3cb	protein phosphatase 3, catalytic subunit, beta isoform	0,82	0,0375
1418815_at	Cdh2	cadherin 2	0,82	0,0479
1425052_at	Isoc1	isochorismatase domain containing 1	0,82	0,0242
1435029_at	NA	NA	0,82	0,0376
1427988_s_at	Safb2	scaffold attachment factor B2	0,83	0,0379
1418584_at	Ccnh	cyclin H	0,83	0,0449
1417241_at	Amz2	archaelysin family metallopeptidase 2	0,83	0,0203
1455205_a_at	Usp19	ubiquitin specific peptidase 19	0,83	0,0337
1427185_at	Mef2a	myocyte enhancer factor 2A	0,83	0,0432
1455958_s_at	Pptc7	PTC7 protein phosphatase homolog (S. cerevisiae)	0,83	0,0211
1436705_at	Mmgt1	membrane magnesium transporter 1	0,84	0,0428
1441646_at	Vta1	Vps20-associated 1 homolog (S. cerevisiae)	0,84	0,0471
1425628_a_at	Gtf2i	general transcription factor II I	0,85	0,0467
1433834_at	Mrz 06	membrane-associated ring finger (C3HC4) 6	0,85	0,0443
1438742_at	Zfp629	zinc finger protein 629	0,85	0,0477

Table III

Differential regulated between Shunt vs. TAC and also significantly regulated to the corresponding Sham

Affymetrix probe set identification	Gene symbol	Gene name	Fold change TAC	Fold change Shunt	Adjusted *P* value TAC vs Shunt
1416342_at	Tnc	tenascin C	8,91	1,93	0,0000
1418219_at	Il15	interleukin 15	0,28	0,61	0,0000
1422168_a_at	Bdnf	brain derived neurotrophic factor	1,60	0,67	0,0000
1425603_at	Tmem176a	transmembrane protein 176A	2,37	1,38	0,0000
1426382_at	Ppm1b	protein phosphatase 1B, magnesium dependent, beta isoform	1,29	0,82	0,0000
1427939_s_at	Mycbp	c-myc binding protein	0,82	1,31	0,0000
1433581_at	1190002N15Rik	RIKEN cDNA 1190002N15 gene	1,43	0,63	0,0000
1433761_at	Pde4dip	phosphodiesterase 4D interacting protein (myomegalin)	1,59	0,65	0,0000
1435029_at	NA	NA	1,17	0,82	0,0001
1435878_at	Stk38l	serine/threonine kinase 38 like	1,22	0,79	0,0000
1447830_s_at	Rgs2	regulator of G-protein signaling 2	0,33	0,63	0,0002
1449396_at	Aoc3	amine oxidase, copper containing 3	0,78	1,32	0,0001
1452649_at	Rtn4	reticulon 4	2,10	1,30	0,0000
1455656_at	Btla	B and T lymphocyte associated	1,40	0,73	0,0000
1460227_at	Timp1	tissue inhibitor of metalloproteinase 1	18,87	2,70	0,0000

Differential regulated between Shunt vs. TAC and between TAC and Sham but not Shunt and Sham

Affymetrix probe set identification	Gene symbol	Gene name	Fold change TAC	Adjusted *P* value TAC vs Shunt
1415690_at	Mrpl27	mitochondrial ribosomal protein L27	0,76	0,0002
1416225_at	Adh1	alcohol dehydrogenase 1 (class I)	0,48	0,0001
1416658_at	Frzb	frizzled-related protein	2,32	0,0001
1417178_at	Gipc2	GIPC PDZ domain containing family, member 2	1,84	0,0001
1417193_at	Sod2	superoxide dismutase 2, mitochondrial	0,84	0,0002
1417214_at	Rab27b	RAB27b, member RAS oncogene family	1,73	0,0002
1417262_at	Ptgs2	prostaglandin-endoperoxide synthase 2	2,48	0,0001
1417311_at	Crip2	cysteine rich protein 2	0,68	0,0002
1417639_at	Slc22a4	solute carrier family 22 (organic cation transporter), member 4	2,41	0,0001
1417675_a_at	Mdn1	midasin homolog (yeast)	1,28	0,0001
1417688_at	Fam20c	family with sequence similarity 20, member C	2,06	0,0000
1417814_at	Pla2g5	phospholipase A2, group V	0,43	0,0002
1418061_at	Ltbp2	latent transforming growth factor beta binding protein 2	4,83	0,0001
1418465_at	Ncf4	neutrophil cytosolic factor 4	2,21	0,0001
1418476_at	Crlf1	cytokine receptor-like factor 1	4,00	0,0001
1418501_a_at	Oxr1	oxidation resistance 1	0,72	0,0002
1418599_at	Col11a1	collagen, type XI, alpha 1	1,70	0,0002
1418729_at	Star	steroidogenic acute regulatory protein	1,62	0,0001
1419132_at	Tlr2	toll-like receptor 2	1,55	0,0002
1419182_at	Svep1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	1,98	0,0001
1419207_at	Zfp37	zinc finger protein 37	1,29	0,0002
1419220_at	Xirp1	xin actin-binding repeat containing 1	2,02	0,0002
1419276_at	Enpp1	ectonucleotide pyrophosphatase/phosphodiesterase 1	3,43	0,0002
1419340_at	Mov10l1	Moloney leukemia virus 10-like 1	0,47	0,0001
1419519_at	Igf1	insulin-like growth factor 1	3,10	0,0001
1419577_at	Fig4	FIG4 homolog (S. cerevisiae)	0,62	0,0002
1419598_at	Ms4a6d	membrane-spanning 4-domains, subfamily A, member 6D	3,67	0,0002
1419599_s_at	Ms4a6d	membrane-spanning 4-domains, subfamily A, member 6D	3,50	0,0002
1419625_at	Hspa1l	heat shock protein 1-like	1,71	0,0001
1419666_x_at	Nupr1	nuclear protein 1	2,12	0,0002
1419994_s_at	D10Ertd641e	DNA segment, Chr 10, ERATO Doi 641, expressed	0,75	0,0002
1420860_at	Itga9	integrin alpha 9	1,48	0,0002
1421075_s_at	Cyp7b1	cytochrome P450, family 7, subfamily b, polypeptide 1	1,54	0,0002
1421186_at	Ccr2	chemokine (C-C motif) receptor 2	1,50	0,0001
1421253_at	Nrap	nebulin-related anchoring protein	1,42	0,0002
1421262_at	Lipg	lipase, endothelial	0,83	0,0001
1422069_at	Mc1r	melanocortin 1 receptor	0,79	0,0002
1422124_a_	Ptprc	protein tyrosine phosphatase, receptor type, C	2,55	0,0001

at				
1422864_at	Runx1	runt related transcription factor 1	2,36	0,0001
1422973_a_at	Thrsp	thyroid hormone responsive SPOT14 homolog (Rattus)	0,57	0,0002
1423250_a_at	Tgfb2	transforming growth factor, beta 2	4,01	0,0001
1423577_at	Ankrd32	ankyrin repeat domain 32	0,49	0,0001
1423615_at	Rnf115	ring finger protein 115	2,14	0,0002
1423760_at	Cd44	CD44 antigen	3,87	0,0001
1424119_at	Prkab1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	0,65	0,0001
1424845_a_at	Cep68	centrosomal protein 68	0,70	0,0002
1425315_at	Dock7	dedicator of cytokinesis 7	1,47	0,0002
1425832_a_at	Cxcr6	chemokine (C-X-C motif) receptor 6	2,26	0,0002
1426541_a_at	Endod1	endonuclease domain containing 1	6,42	0,0002
1426604_at	Rnasel	ribonuclease L (2', 5'-oligoisoadenylate synthetase-dependent)	1,77	0,0002
1426909_at	Uck2	uridine-cytidine kinase 2	3,38	0,0000
1427076_at	Mpeg1	macrophage expressed gene 1	1,82	0,0001
1427213_at	Pfkfb1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	0,35	0,0001
1427582_at	Fgf6	fibroblast growth factor 6	2,50	0,0001
1427966_at	Fam105b	family with sequence similarity 105, member B	1,95	0,0001
1428589_at	Mrpl41	mitochondrial ribosomal protein L41	0,84	0,0002
1428902_at	Chst11	carbohydrate sulfotransferase 11	1,44	0,0001
1429178_at	Odz3	odd Oz/ten-m homolog 3 (Drosophila)	1,56	0,0002
1429549_at	Col27a1	collagen, type XXVII, alpha 1	1,35	0,0002
1429768_at	Dtna	dystrobrevin alpha	1,55	0,0001
1430695_at	Tlr4	toll-like receptor 4	2,20	0,0001
1430786_at	1110002E22Rik	RIKEN cDNA 1110002E22 gene	2,07	0,0001
1431293_a_at	Cldnd1	claudin domain containing 1	2,08	0,0002
1433434_at	AW551984	expressed sequence AW551984	1,79	0,0000
1433857_at	Fat1	FAT tumor suppressor homolog 1 (Drosophila)	1,60	0,0002
1433982_at	Usp28	ubiquitin specific peptidase 28	1,69	0,0001
1434239_at	Rrp12	ribosomal RNA processing 12 homolog (S. cerevisiae)	1,98	0,0001
1434376_at	Cd44	CD44 antigen	2,74	0,0001
1434447_at	Met	met proto-oncogene	1,65	0,0002
1434672_at	Gpr22	G protein-coupled receptor 22	0,17	0,0002
1435149_at	Plcg1	phospholipase C, gamma 1	0,79	0,0002
1435331_at	Pyhin1	pyrin and HIN domain family, member 1	1,56	0,0002
1435585_at	Tceal7	transcription elongation factor A (SII)-like 7	2,74	0,0001
1435588_at	Wdfy1	WD repeat and FYVE domain containing 1	1,51	0,0001
1436329_at	Egr3	early growth response 3	6,91	0,0002
1436336_at	Ptrh1	peptidyl-tRNA hydrolase 1 homolog (S. cerevisiae)	1,50	0,0001
1436870_s_at	Afap1l2	actin filament associated protein 1-like 2	1,91	0,0002
1436937_at	Rbms3	RNA binding motif, single stranded interacting protein	1,74	0,0001
1437009_a_at	Rnf115	ring finger protein 115	2,19	0,0001
1437218_at	Fn1	fibronectin 1	2,29	0,0001
1437284_at	Fzd1	frizzled homolog 1 (Drosophila)	1,94	0,0002

1438195_at	Gpd1l	glycerol-3-phosphate dehydrogenase 1-like	0,64	0,0002
1438303_at	Tgfb2	transforming growth factor, beta 2	1,74	0,0001
1438638_x_at	Fam116b	family with sequence similarity 116, member B	0,76	0,0002
1439168_at	Camk2d	calcium/calmodulin-dependent protein kinase II, delta	2,03	0,0001
1439352_at	Trim7	tripartite motif-containing 7	0,51	0,0001
1439740_s_at	Uck2	uridine-cytidine kinase 2	5,30	0,0000
1440351_at	NA	NA	1,70	0,0001
1440563_at	NA	NA	1,79	0,0001
1440729_at	Eps15	epidermal growth factor receptor pathway substrate 15	2,01	0,0002
1440771_at	Zkscan1	zinc finger with KRAB and SCAN domains 1	1,64	0,0001
1440878_at	Runx1	runt related transcription factor 1	1,66	0,0002
1441063_at	Eif2c3	eukaryotic translation initiation factor 2C, 3	1,62	0,0002
1441137_at	Bicc1	bicaudal C homolog 1 (Drosophila)	1,61	0,0001
1441792_at	A630033E08 Rik	RIKEN cDNA A630033E08 gene	1,25	0,0001
1441826_x_at	NA	NA	0,77	0,0002
1442251_at	Vcpip1	valosin containing protein (p97)/p47 complex interacting protein 1	1,66	0,0001
1442849_at	Lrp1	low density lipoprotein receptor-related protein 1	1,38	0,0001
1444031_at	Camk2d	calcium/calmodulin-dependent protein kinase II, delta	2,98	0,0001
1444058_at	Dzip3	DAZ interacting protein 3, zinc finger	3,45	0,0001
1444361_at	Ap1s2	adaptor-related protein complex 1, sigma 2 subunit	1,47	0,0001
1444537_at	AI429363	expressed sequence AI429363	1,67	0,0002
1445576_at	Rsph10b2	radial spoke head 10 homolog B (Chlamydomonas)	0,84	0,0002
1446324_at	NA	NA	1,52	0,0001
1447812_x_at	Flnc	filamin C, gamma	2,40	0,0000
1447819_x_at	Col8a1	collagen, type VIII, alpha 1	5,81	0,0001
1447870_x_at	1110002E22 Rik	RIKEN cDNA 1110002E22 gene	1,83	0,0001
1448065_at	NA	NA	0,73	0,0002
1448130_at	Fdft1	farnesyl diphosphate farnesyl transferase 1	0,45	0,0001
1448467_a_at	Ehbp1l1	EH domain binding protein 1-like 1	1,25	0,0002
1448604_at	Uck2	uridine-cytidine kinase 2	4,37	0,0001
1448617_at	Cd53	CD53 antigen	2,10	0,0001
1449073_at	Flnc	filamin C, gamma	2,46	0,0000
1449154_at	Col11a1	collagen, type XI, alpha 1	2,38	0,0000
1449175_at	Gpr65	G-protein coupled receptor 65	2,05	0,0002
1449254_at	Spp1	secreted phosphoprotein 1	53,75	0,0000
1450311_at	Slc8a3	solute carrier family 8 (sodium/calcium exchanger), member 3	0,78	0,0002
1450922_a_at	Tgfb2	transforming growth factor, beta 2	4,21	0,0000
1450923_at	Tgfb2	transforming growth factor, beta 2	3,24	0,0000
1450984_at	Tjp2	tight junction protein 2	1,64	0,0002
1451175_at	Spcs3	signal peptidase complex subunit 3 homolog (S. cerevisiae)	1,72	0,0002
1451227_a_at	Slc10a3	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	1,63	0,0002
1451716_at	Mafb	v-maf musculoaponeurotic fibrosarcoma oncogene	1,75	0,0001

		family, protein B (avian)		
1451939_a_at	Srpx	sushi-repeat-containing protein	2,63	0,0001
1452086_at	Trmt5	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae)	0,41	0,0001
1452286_at	Slain2	SLAIN motif family, member 2	1,31	0,0001
1452417_x_at	LOC100047628	similar to Chain L, Structural Basis Of Antigen Mimicry In A Clinically Relevant Melanoma Antigen System	2,34	0,0002
1452968_at	Cthrc1	collagen triple helix repeat containing 1	4,61	0,0001
1453355_at	Wnk2	WNK lysine deficient protein kinase 2	0,47	0,0001
1454995_at	Ddah1	dimethylarginine dimethylaminohydrolase 1	2,26	0,0002
1455280_at	Frem1	Fras1 related extracellular matrix protein 1	2,03	0,0001
1455374_at	Kcnj3	potassium inwardly-rectifying channel, subfamily J, member 3	0,38	0,0001
1455660_at	Csf2rb	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	2,15	0,0001
1455833_at	Afap1l2	actin filament associated protein 1-like 2	1,34	0,0002
1456357_at	A930041I02Rik	RIKEN cDNA A930041I02 gene	1,58	0,0001
1456611_at	Fam13a	family with sequence similarity 13, member A	1,40	0,0002
1456777_at	Mgam	maltase-glucoamylase	2,31	0,0001
1456887_at	Cmklr1	chemokine-like receptor 1	1,36	0,0002
1457022_at	NA	NA	1,56	0,0001
1457271_at	Gm131	gene model 131, (NCBI)	0,77	0,0001
1457296_at	Cilp	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	7,11	0,0002
1457980_x_at	Uck2	uridine-cytidine kinase 2	2,37	0,0001
1459090_at	NA	NA	0,73	0,0002
1459350_at	NA	NA	1,71	0,0001
1459457_at	Camk2d	calcium/calmodulin-dependent protein kinase II, delta	2,08	0,0001
1459546_s_at	Enpp1	ectonucleotide pyrophosphatase/phosphodiesterase 1	2,86	0,0001
1459637_at	NA	NA	0,74	0,0001
1460133_at	NA	NA	1,44	0,0001
1460218_at	Cd52	CD52 antigen	2,70	0,0001

Differential regulated between Shunt vs. TAC and between Shunt and Sham but not TAC and Sham

Affymetrix probe set identification	Gene symbol	Gene name	Fold change Shunt	Adjusted *P* value TAC vs Shunt
1415999_at	Hey1	hairy/enhancer-of-split related with YRPW motif 1	1,84	0,0002
1420715_a_at	Pparg	peroxisome proliferator activated receptor gamma	1,42	0,0001
1426759_at	Map4k3	mitogen-activated protein kinase kinase kinase kinase 3	1,24	0,0001
1428452_at	2810025M15Rik	RIKEN cDNA 2810025M15 gene	1,25	0,0002
1428554_a_at	1810035L17Rik	RIKEN cDNA 1810035L17 gene	1,29	0,0001
1428976_at	Tmpo	thymopoietin	1,55	0,0001
1429315_at	Syt11	synaptotagmin XI	0,77	0,0002
1431126_a_at	0610011F06Rik	RIKEN cDNA 0610011F06 gene	0,59	0,0001
1433992_at	Shroom2	shroom family member 2	2,51	0,0001
1434684_at	Rin3	Ras and Rab interactor 3	1,47	0,0001
1435737_a_at	Nde1	nuclear distribution gene E homolog 1 (A nidulans)	1,34	0,0002
1435905_at	D3Ertd300e	DNA segment, Chr 3, ERATO Doi 300, expressed	0,73	0,0001
1439015_at	Gfra1	glial cell line derived neurotrophic factor family receptor alpha 1	0,51	0,0001
1439511_at	Cdk7	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	0,58	0,0002
1441577_at	C530014P21Rik	RIKEN cDNA C530014P21 gene	0,60	0,0000
1446528_at	Scyl2	SCY1-like 2 (S. cerevisiae)	0,74	0,0002
1451257_at	Acsl6	acyl-CoA synthetase long-chain family member 6	1,45	0,0002
1453646_at	3110005L21Rik	RIKEN cDNA 3110005L21 gene	0,63	0,0002
1455459_at	Prdm15	PR domain containing 15	0,58	0,0002
1455817_x_at	Zxdb	zinc finger, X-linked, duplicated B	0,74	0,0002
1457338_at	NA	NA	0,53	0,0001
1459048_s_at	Zfp142	zinc finger protein 142	0,67	0,0001

Table IV

Pathways activated in TAC

ID	Name	*P* value
X00040	Pentose and glucuronate interconversions	0,014
X00361	gamma-Hexachlorocyclohexane degradation	0,014
X00512	O-Glycan biosynthesis	0,014
X00531	Glycosaminoglycan degradation	0,014
X00532	Chondroitin sulfate biosynthesis	0,014
X00603	Glycosphingolipid biosynthesis - globo series	0,014
X00604	Glycosphingolipid biosynthesis - ganglio series	0,014
X00983	Drug metabolism - other enzymes	0,014
X01032	Glycan structures - degradation	0,014
X03010	Ribosome	0,014
X03030	DNA replication	0,014
X03410	Base excision repair	0,014
X03420	Nucleotide excision repair	0,014
X03430	Mismatch repair	0,014
X04110	Cell cycle	0,014
X04115	p53 signaling pathway	0,014
X04210	Apoptosis	0,014
X04510	Focal adhesion	0,014
X04512	ECM-receptor interaction	0,014
X04514	Cell adhesion molecules (CAMs)	0,014
X04520	Adherens junction	0,014
X04530	Tight junction	0,014
X04620	Toll-like receptor signaling pathway	0,014
X04650	Natural killer cell mediated cytotoxicity	0,014
X04660	T cell receptor signaling pathway	0,014
X04662	B cell receptor signaling pathway	0,014
X04670	Leukocyte transendothelial migration	0,014
X04810	Regulation of actin cytoskeleton	0,014
X05014	Amyotrophic lateral sclerosis (ALS)	0,014
X05040	Huntington's disease	0,014
X05050	Dentatorubropallidoluysian atrophy (DRPLA)	0,014
X05060	Prion disease	0,014
X05210	Colorectal cancer	0,014
X05214	Glioma	0,014
X05215	Prostate cancer	0,014
X05218	Melanoma	0,014
X05222	Small cell lung cancer	0,014
X05322	Systemic lupus erythematosus	0,014
X04940	Type I diabetes mellitus	0,024
X05332	Graft-versus-host disease	0,024

Pathways repressed in TAC

ID	Name	*P* value
X00010	Glycolysis / Gluconeogenesis	0,014
X00020	Citrate cycle (TCA cycle)	0,014
X00030	Pentose phosphate pathway	0,014
X00051	Fructose and mannose metabolism	0,014
X00071	Fatty acid metabolism	0,014
X00120	Bile acid biosynthesis	0,014
X00190	Oxidative phosphorylation	0,014
X00220	Urea cycle and metabolism of amino groups	0,014
X00230	Purine metabolism	0,014
X00251	Glutamate metabolism	0,014
X00252	Alanine and aspartate metabolism	0,014
X00260	Glycine, serine and threonine metabolism	0,014
X00271	Methionine metabolism	0,014
X00272	Cysteine metabolism	0,014
X00280	Valine, leucine and isoleucine degradation	0,014
X00290	Valine, leucine and isoleucine biosynthesis	0,014
X00310	Lysine degradation	0,014
X00340	Histidine metabolism	0,014
X00350	Tyrosine metabolism	0,014
X00360	Phenylalanine metabolism	0,014
X00380	Tryptophan metabolism	0,014
X00410	beta-Alanine metabolism	0,014
X00450	Selenoamino acid metabolism	0,014
X00480	Glutathione metabolism	0,014
X00561	Glycerolipid metabolism	0,014
X00563	Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	0,014
X00564	Glycerophospholipid metabolism	0,014
X00565	Ether lipid metabolism	0,014
X00592	alpha-Linolenic acid metabolism	0,014
X00620	Pyruvate metabolism	0,014
X00630	Glyoxylate and dicarboxylate metabolism	0,014
X00632	Benzoate degradation via CoA ligation	0,014
X00640	Propanoate metabolism	0,014
X00650	Butanoate metabolism	0,014
X00790	Folate biosynthesis	0,014
X00860	Porphyrin and chlorophyll metabolism	0,014
X00903	Limonene and pinene degradation	0,014
X00910	Nitrogen metabolism	0,014
X00960	Alkaloid biosynthesis II	0,014
X00970	Aminoacyl-tRNA biosynthesis	0,014
X00980	Metabolism of xenobiotics by cytochrome P450	0,014
X00982	Drug metabolism - cytochrome P450	0,014
X01031	Glycan structures - biosynthesis 2	0,014
X01040	Biosynthesis of unsaturated fatty acids	0,014
X02010	ABC transporters - General	0,014
X03020	RNA polymerase	0,014
X03060	Protein export	0,014
X03320	PPAR signaling pathway	0,014
X04020	Calcium signaling pathway	0,014
X04120	Ubiquitin mediated proteolysis	0,014
X04140	Regulation of autophagy	0,014

X04340	Hedgehog signaling pathway	0,014
X04614	Renin-angiotensin system	0,014
X04664	Fc epsilon RI signaling pathway	0,014
X04910	Insulin signaling pathway	0,014
X04920	Adipocytokine signaling pathway	0,014
X04930	Type II diabetes mellitus	0,014
X05010	Alzheimer's disease	0,014
X05012	Parkinson's disease	0,014
X00533	Keratan sulfate biosynthesis	0,022

Table V

Pathways activated in Shunt

ID	Name	*P* value
X00040	Pentose and glucuronate interconversions	0,014
X04310	Wnt signaling pathway	0,014
X04520	Adherens junction	0,014
X04810	Regulation of actin cytoskeleton	0,014
X04916	Melanogenesis	0,014
X05040	Huntington's disease	0,014
X05050	Dentatorubropallidoluysian atrophy (DRPLA)	0,014

Not present in the TAC model

Pathways repressed in Shunt

ID	Name	*P* value
X00252	Alanine and aspartate metabolism	0,014
X00280	Valine, leucine and isoleucine degradation	0,014
X00290	Valine, leucine and isoleucine biosynthesis	0,014
X00450	Selenoamino acid metabolism	0,014
X04140	Regulation of autophagy	0,014
X04612	Antigen processing and presentation	0,014
X05340	Primary immunodeficiency	0,024

Not present in the TAC model